

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: January 15, 2004, 06:08:59 ; Search time 2613 Seconds
(without alignments)
1807.571 Million cell updates/sec

Title: US-09-809-545a-1
Perfect score: 1340
Sequence: 1 GCGGCGCGCCGACACAAAT.....GGCGGAGGAGGTCGCTAGA 1340

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2324096 seqs, 1762381658 residues

Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA.*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1340	100.0	1340	10	US-09-809-545a-1	Sequence 1, Appli
2	857.2	64.0	2372	9	US-09-794-591-1	Sequence 1, Appli
3	275.6	20.6	1506	13	US-10-359-385-5	Sequence 5, Appli
4	274	20.4	1558	13	US-10-094-749-287	Sequence 287, App
5	261	19.5	1843	11	US-09-919-039-266	Sequence 266, App
6	123.8	9.2	473	9	US-09-864-761-11804	Sequence 11804, A
7	109.6	8.2	125	9	US-09-864-761-28375	Sequence 28375, A
8	90.4	6.7	255	13	US-10-029-386-26399	Sequence 26399, A
9	90.4	6.7	255	13	US-10-029-386-12653	Sequence 12653, A
10	88	6.6	224	9	US-09-864-761-22653	Sequence 22653, A
11	86.4	6.4	454	9	US-09-864-761-5893	Sequence 5893, App
12	58	4.3	2350	12	US-10-292-798-1837	Sequence 1837, App
13	58	4.3	2350	13	US-10-017-161-2191	Sequence 2191, App
14	57	4.3	65	13	US-09-908-975-27923	Sequence 27923, A
15	55.8	4.2	6668	13	US-10-311-455-1669	Sequence 1669, App

16	55.2	4.1	60	13	US-09-908-975-7420	Sequence 7420, App
17	55.2	4.1	3001	15	US-10-172-086-57	Sequence 57, Appl
18	55.2	4.1	4722	13	US-10-311-455-2037	Sequence 2037, App
19	53.6	4.0	9539	13	US-10-240-453-54	Sequence 54, Appl
20	53.6	4.0	9539	13	US-10-239-676-52	Sequence 52, Appl
21	53.4	4.0	5464	13	US-10-311-455-1889	Sequence 1889, App
22	53	4.0	1223197	13	US-10-027-632-179264	Sequence 179264, A
23	53	4.0	1223197	14	US-10-027-632-179264	Sequence 53, Appl
24	52.8	3.9	396	9	US-09-825-294-53	Sequence 53, Appl
25	52.8	3.9	396	10	US-09-970-966-53	Sequence 53, Appl
26	52.8	3.9	396	12	US-10-369-186-53	Sequence 53, Appl
27	52.8	3.9	396	12	US-10-361-811-53	Sequence 53, Appl
28	52.8	3.9	396	16	US-10-212-677-53	Sequence 53, Appl
29	52.6	3.9	113515	13	US-10-311-455-2148	Sequence 2148, App
30	52.6	3.9	393	10	US-09-960-352-4582	Sequence 4582, App
31	52	3.9	4237	9	US-09-745-763-20	Sequence 20, Appli
32	52	3.9	3673778	13	US-10-312-841-2	Sequence 2, Appli
33	51.6	3.9	461	11	US-09-918-995-16144	Sequence 16144, A
34	51.6	3.9	495	11	US-09-918-995-32216	Sequence 32216, A
35	51.2	3.8	1347	15	US-10-128-714-7140	Sequence 7140, App
36	51	3.8	5314	13	US-10-311-455-134	Sequence 134, App
37	51	3.8	5314	13	US-10-240-452-10	Sequence 10, Appl
38	51	3.8	8305	13	US-10-311-455-1541	Sequence 1541, App
39	51	3.8	8342	13	US-10-311-455-474	Sequence 474, App
40	51	3.8	113515	12	US-10-311-455-2147	Sequence 2147, App
41	51	3.8	165961	12	US-10-085-117-241	Sequence 241, App
42	50.4	3.8	3973	13	US-10-311-455-144	Sequence 144, App
43	50.4	3.8	16033	13	US-10-311-455-1377	Sequence 1377, App
44	50.4	3.8	17934	13	US-10-311-455-1692	Sequence 1692, App
45	50	3.7	16167	13	US-10-311-455-1056	Sequence 1056, App

ALIGNMENTS

RESULT 1
US-09-809-545a-1
; Sequence 1, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; APPLICANT: White, R. Tyler
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS. 017A
; CURRENT APPLICATION NUMBER: US/09/809, 545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1340
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-09-809-545a-1

Query Match 100.0%; Score 1340; DB 10; Length 1340;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GCGGCGCGCCGACACAAATGCTGAGCTTATGCTCAGCGGAGTTCGTCACCCCA	60
DB	1	GCGGCGCGCCGACACAAATGCTGAGCTTATGCTCAGCGGAGTTCGTCACCCCA	60
QY	61	ATGGGATCGCTGAGATACAGCGCCCTCATCCCATCCCGGCGGAGAGACACCGGCGAG	120
DB	61	ATGGGATCGCTGAGATACAGCGCCCTCATCCCATCCCGGCGGAGAGACACCGGCGAG	120
QY	121	CCCACTGTCGCCGACACATTAATCTGATCTCTACACAGAGCACTCGAGACAGAG	180
DB	121	CCCACTGTCGCCGACACATTAATCTGATCTCTACACAGAGCACTCGAGACAGAG	180
QY	181	CGCTTATACAGCGGACGCTCTCCGCGACCGGACACAGACAGATGATCCCGCCCG	240
DB	181	CGCTTATACAGCGGACGCTCTCCGCGACCGGACACAGACAGATGATCCCGCCCG	240

QY 241 ACCGACGGCCAGCCGAGACACCACTTCTGAAAAACAGAAAAAAGTCCAGCCCAAG 300
 Db 241 ACCGACGGCCAGCCGAGACACCACTTCTGAAAAACAGAAAAAAGTCCAGCCCAAG 300
 QY 301 CGGCTCATGTGTCCAAACATCCCTTCGCGTTCGCGATCCAGACTCCGACAAATGTTT 360
 Db 301 CGGCTCATGTGTCCAAACATCCCTTCGCGTTCGCGATCCAGACTCCGACAAATGTTT 360
 QY 361 GGGCAATTTGGTAAATATTAATGATTTTAAATTTTAAATGAGGGGCTGAAAGGGA 420
 Db 361 GGGCAATTTGGTAAATATTAATGATTTTAAATTTTAAATGAGGGGCTGAAAGGGA 420
 QY 421 TTTGGTTTGTGTAATTTGAAAAATAGTGGATGCGGACAGGGCGAGGAATTTGAC 480
 Db 421 TTTGGTTTGTGTAATTTGAAAAATAGTGGATGCGGACAGGGCGAGGAATTTGAC 480
 QY 481 GGTACCGTGTAGAGGGCGGTAAATTCAGGTTAATTAATGCGACAGACGCGTGTACT 540
 Db 481 GGTACCGTGTAGAGGGCGGTAAATTCAGGTTAATTAATGCGACAGACGCGTGTACT 540
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 Db 541 AATTAAGGCGCTGAAACCCCTTACCAATGCTGGAATTAATTAATGAGGGGCGG 600
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 QY 721 TATCCGCGCCGCTGCTGTGACAGTGTACACGAGGGCTCACTTTCAGGCGGTGTCG 780
 Db 721 TATCCGCGCCGCTGCTGTGACAGTGTACACGAGGGCTCACTTTCAGGCGGTGTCG 780
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 Db 781 ACCGTGTACAAACCTTCAAGAGTGGCGGCGCCCAACCCCAATCCGCGCTATGCGGA 840
 QY 841 GTAAGTATCAAGAGCAGTGTATGAGCAATTAATTTGCTACAGGGTGTACGCTGATAC 900
 Db 841 GTAAGTATCAAGAGCAGTGTATGAGCAATTAATTTGCTACAGGGTGTACGCTGATAC 900
 QY 901 CGCTACGCGCCAGCCCACTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
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 QY 1201 ACCTTCCAAATGTGGGAGAGAGAGCTTTCCGAGGCCGAGTGTGCAACATGAGT 1260
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 Db 1261 AGGACATCATCTTTAGCAACTCAAGAAACAAAGAAAAAATTAAGC 1320

QY 1321 GGCCGAAAGGGTTCGCTAGA 1340
 Db 1321 GGCCGAAAGGGTTCGCTAGA 1340
 RESULT 2
 US-09-794-591-1
 ; Sequence 1, Application US/09794591
 ; Patent No. US20010018198A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pulst, Stefan M.
 ; APPLICANT: Shiba, Hiroki
 ; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
 ; TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
 ; FILE REFERENCE: CE 3093
 ; CURRENT APPLICATION NUMBER: US/09/794,591
 ; PRIOR FILING DATE: 1998-09-01
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 2372
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (987)..(1979)
 US-09-794-591-1
 Query Match 64.0%; Score 857.2; DB 9; Length 2372;
 Best Local Similarity 82.7%; Pred. No. 2e-232;
 Matches 1141; Conservative 0; Mismatches 138; Indels 101; Gaps 10;
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 Db 1029 GCGCGCCCGCCGACCAATGGCTCAG-CTTAAGCCCTACAGGAGGAGTTGCTCACCCCAAG 1088
 QY 60 AATGCAATCTT-SCAATATACAGGCGCCCTCATCCCATCCCGCGCAGAG-ACACCGGC 117
 Db 1089 AATGCAATCTT-SCAATATACAGGCGCCCTCATCCCATCCCGCGCAGAG-ACACCGGC 1148
 QY 118 CAGCCCACTGTCCCG-CCACATTAATCTTG-ATCTCTTACACAGAGCCTCGAG 175
 Db 1149 CAGCCCACTGTCCCG-CCACATTAATCTTG-ATCTCTTACACAGAGCCTCGAG 1208
 QY 176 CAGAGC---GCTATACAGGCGCAG-CCGTCTCCGCGACCGGCAACAGACAGATAT 231
 Db 1209 CAGAGC---GCTATACAGGCGCAG-CCGTCTCCGCGACCGGCAACAGACAGATAT 1268
 QY 232 GCCGCCCGACGAGCGCCAGCCGACACAACTTCTGAAAAACAGAAAAAAGTCC 291
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 QY 352 CAATATTTGGCCAAATTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 411
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 QY 472 AAATTCACGCTACCGTGTGAGAGGCGGTAATTCAGGTTAATTAATTCAGACGCG 531
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 QY 532 GTGATGACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 591
 Db 1569 GTGATGACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1628

Qy	592	GTGGGCGGGGCTACAGGCCCGGACCTTCTATGAGGACAGGGTCTGTGGCCAGGGCAAC	651
Db	1629	GTGGGTGACGCTCAAGTCCCGAATCTTATGACGACAGGTCCTGTGTGCCAGGCAAC	1688
Qy	652	CAGAGGGATCTTCCATGTACAGTGGGCCCAAGTTCATTGTATATACTTGTGCATGTCT	711
Db	1689	CAGAGGGATCTTCCATGTACAGTGGGCCCAAGTTCATTGTATATACTTGTGCATGTCA	1748
Qy	712	GGCTTTCATATCCGGCCGCCACTGCTGTGATGCAATCCAGGGGCTCACCTTGAAGGC	771
Db	1749	GGCTTTCATATCCGGCCGCCACTGCTGTGATGCAATCCAGGGGCTCACCTTGAAGGC	1808
Qy	772	CGTGGTGCACCGGTGTACACACCTTCAAGGTGGGAGGCCCCCAATCCCGGCTC	831
Db	1809	CGCGGTGCACCGGTGTACACACCTTCAAGGGCGGGGAGGCCCCCAATCCCGGCTC	1868
Qy	832	TATGGCGGAGTAGTGTATCAAGGCGCAAGTGTATGGAATTAATGCTACAGGGTGTTC	891
Db	1869	TACGGCGGAGTAGTGTATCAAGGCGCAAGTGTATGGAATTAATGCTACAGGGTGTTC	1926
Qy	892	GCTGCTATCCGGTATAGGCCCAAGCCCACTGCTGTGCTGTGCTTACATGGA-----	944
Db	1927	GCTGCTATCCGGTATAGGCCCAAGCCCACTGCTGTGCTGTGCTTACATGGA-----	1986
Qy	945	-----CAGTTACGGACGAG	958
Db	1987	CAGTTACGGACGAG-----CAGTTACGGACGAG	2046
Qy	959	TTTATGCTGCGGACCCCTTACGACCAACACACTTGTCTCAAGCCGCCCACTACGGCTGTG	1018
Db	2047	TTTATGCTGCGGACCCCTTACGACCAACACACTTGTCTCAAGCCGCCCACTACGGCTGTG	2106
Qy	1019	CCATGAATGCTTTTGGCGGCTTGAACCATGCGCAAGACTTGAAGAGCATGCTGATGATGG	1078
Db	2107	CCATGAATGCTTTTGGCGGCTTGAACCATGCGCAAGACTTGAAGAGCATGCTGATGATGG	2166
Qy	1079	GTCCTGTTCTTCTTCATTGTGACGCTAGTATATACCAAGGGGAGATCAACCGTTTGTCT	1138
Db	2167	GTCCTGTTCTTCTTCATTGTGACGCTAGTATATACCAAGGGGAGATCAACCGTTTGTCT	2226
Qy	1139	CATATTAATGATTAACCATTTAAACAAACAGCAAAAAACAAAAACAAAAAAC	1198
Db	2227	CATATTAATGATTAACCATTTAAACAAACAGCAAAAAACAAAAACAAAAAAC	2250
Qy	1199	CAACCTTCATATGCGGGAGAGAGACCTTTCGAGGCCCGAGTGTTCGACACATGCA	1258
Db	2251	-AACCTTCATATGCGGGAGAGAGACCTTTCGAGGCCCGAGTGTTCGACACATGCA	2309
Qy	1259	GTAGAGACATCACTTATGCACTCAAAAGAAACACGAAAAAATTTTTAAAAATTTA	1318
Db	2310	GTAGAGACATCACTTATGCACTCAAAAGAAACACGAAAAAATTTTTAAAAATTTA	2369
RESULT 3			
US-10-359-385-5			
Sequence 5, Application US/10359385			
Publication No. US20030143622A1			
GENERAL INFORMATION:			
APPLICANT: Bandman, Olga			
APPLICANT: Tang, Y. Tom			
APPLICANT: Corley, Neil C.			
APPLICANT: Guegler, Karl J.			
APPLICANT: Lu, Aina			
APPLICANT: Baughn, Mariah R.			
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS			
FILE REFERENCE: PR-0611 US			
CURRENT APPLICATION NUMBER: US/10/359,385			
CURRENT FILING DATE: 2003-02-05			
PRIOR APPLICATION NUMBER: US/09/176,657			
PRIOR FILING DATE: 1998-10-21			
NUMBER OF SEQ. ID NOS: 9			
SOFTWARE: PERL Program			

[illegible]

Db 1327 CAGTTTCATGAGCCCTGGCTATTGCATATTTTACTAGTAGAGAACTTATACGAGATGA 1386
 Oy 1164 CAACACAGCAAAAAACAACAAAAACAAAAACCA 1201
 Db 1387 AGAGAAAAACAACAAACAACAAACAAAAACACAA 1424

RESULT 4

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US-10-094-749-287
; Sequence 287, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: MAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FILM-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094, 749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350, 435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 287
; LENGTH: 1558
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-094-749-287

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Query Match	20.4%	Score 274;	DB 13;	Length 1558;
Best Local Similarity	65.2%	Pred. No. 6.6e-67;		
Matches 558; Conservative	0;	Mismatches 235;	Indels 63;	Gaps 8

Oy	222	GACAGATGATCGCGCCCGACCGACGGCCAGC---	CCGAGACACAACCTTGTGAAAACAC	278
Db	538	GACAGAAGTGGAGACACAGACGCGCAGCAGTCA	CAGACACAAGAAGTAGTGAATAATTC	597
Oy	279	AGAAAACAAGTCCACGCCCAAGCGGCTGCATGT	GTCCAAACATCCCTTCCGGTTCGGGGA	338
Db	598	AGAGGTAAATCTACCCGAAACGGCTGCATGTCT	TAATATTCATTTCCGTTCCGGGA	657
Oy	339	TCCAGACCTCCGACCAATGTTTGGCCAAATTTG	TAAATATATAGATGTTGAAATATTTT	398
Db	658	CCCTGACCTCCGGGACAGATGTTTGGCAGATTT	GGCAAAATCCTAAGATGTAATATATCTT	717
Oy	399	TAAATGACGGGGCTGAAAGGGATTTGGTTTGT	TAATCTTGAAATATGTGCGGATGCGGA	458
Db	718	TAAATGAAGTGGCTCTTAAAGGATTCGGGTTCT	TAACTTTGCGAAATAGTGTGATGTCAGA	777
Oy	459	CAGGCGCAGGAGAAATTGCACGCTACCGTGTAG	AGGCGCCTAAATCTCAGAGTAAATPA	518
Db	778	CAGGCGCCAGGAGAAATTACACGGCACCGTGGT	TAAAGGCGCCTAAATCTGAGGTGAATPA	837
Oy	519	TGCGACAGCACGCGTGAATGACTTAATPAAAAG	CGCTGAACCCCTTACCAATGCGCTGGAA	578

Db	838	TGCTACAGCAGCGTGTATATGACCAATAAGAAATGTGTACACACCATATGCAATATGTTGGAA	897
Qy	579	ATTAAATCCAGTGTGTGGGCGCGGTCTACAGCCCCGACTTGTATAGCAG-----GCA	628
Db	898	ATTAAAGCCAGTATAGTGGAGCTGTATATGTGTCCGAGATTATATGACAGATTCAGCTTTCA	957
Qy	629	CGGTGCTGTGTGTGACAGGCCAACACAGAGGAGATCTTCATGTAT-----CAG	674
Db	958	AGCAGATGTGTCCCTTAGGCACATGATGACAGATGCCCTCTATCAGAAAGAGGGGTATCA	1017
Qy	675	TGGGCCAGTTTCACCTGTATATATCTTTCGCAATGCTGTGCTTTCCATA---TCGCGCGC	731
Db	1018	CACCTAATATCTTTATACAGTCTCCCTTTAGTTTCCTGCGCTTCCTTACCTTACCTGAGC	1077
Qy	732	CACGTGTCAGCTGCATATCCGAGGGGTCACTTTCAGAGCCGTGTGTGCACCTGTACAA	791
Db	1078	CACCACGGACGCGCTTTCAGAGGAGCCCATTTGAGGGGACAGGGGCGGACAGATATGTG	1137
Qy	792	CACCTTACAGCTGTGGGCGGCCCCACCCCCCAATCCGCGCTTATGCGGAGATAGTATCA	851
Db	1138	TGCAGTCCGA---GCGGTACCTCCAAAGCAGATCCCGCTTATCCAGTGTGTTTACCA	1194
Qy	852	AGAGCCAGTGTATATGGCAATAATTTGTCTACAGGGTGTATTACGTGCATACCGTACGCCCA	911
Db	1195	GGACGAGATTTTATCGGTCTGA---CCTCTATGTGTGATATGCAAGCTTACAGATATGACA	1251
Qy	912	GCCCAACCCCT-----GCCACTGTCTGTGCTTACAGTGCAG	947
Db	1252	GCCTGTACATCGCAACGCGACGACACCGGTGTGTGACGCGGTGACGCGCTTACGGTGA	1311
Qy	948	TTTACGCAAGATTATATCTGTGCGAACCCTTACACACACACACTTGTCTCAAGCCCCCACTTA	1007
Db	1312	TTTATGGCAGGGTGTACACAGCCGACCCCT---ACATAGCTCTTGCCTTCGCTCAGTACTTA	1368
Qy	1008	CGGCTTGTGTGCATG	1023
Db	1369	TGAGATTGGCGCTGTG	1384

RESULT 5

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US-09-919-039-266
; Sequence 266, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaest, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 266
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 253783.3
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1824
; OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-266

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Query Match	19.5%	Score 261	DB 11	Length 1843
Best Local Similarity	68.8%	Pred. No. 3	6e-63	
Best Match 433	Conservative	0	Mismatches 185	Indels 11
				Gaps 5

QY 34 CCTCAGGCGAGTTGGCTCCACCCGAGATGGCAT - CCTGCAGATACAGGCCCCCTATC 92
DB 716 CCGCGCAGTACCCCCCTCCGCGACAGACGCAATCCCTGCGAGTACGCCCGGCCCCAC 775

QY	93	CCCAATCCCGGCGCAGA -GACACCGGCGCAGGCCCATGTGCCCC-----GCCACACATTAAAC	146
Db	776	CGCACCCACCCAGAGACTTACTTCGCGCCAGACCCCGGTGCCCAACAGCATGCAAGACC	835
QY	147	TTGATCTCTTACACAGACGCACTTCGAGCAG--AGCGCTTATTAACAAGCGACAG-CCG	202
Db	836	TGTACACACACAGACAGACCCACCCCGAGCAGCGCTCGAGGGCCAGCACACAGCCCA	895
QY	203	TCTCCGGAACCGGCCACACAGACAGTGTATGCTCCGCCCGACCGAGCGGCCACCGACAC	262
Db	896	TCGCGCGGAGCCAGACAGTGCCTCGCAGACAGAGCGGCGCACAGCGACAGCCAGCCGC	955
QY	263	AACCTTGGAAAAACAGAAAAACAAGTCCCAAGCCCAAGCGGCTGCATGTGTCACATCC	322
Db	956	TCACACCTCCGACCTTACAGAGAGCAGCAGCCCAAGCGGCTTACATGCTTCCACATCC	1015
QY	323	CCCTCCGGTCCGGGATCCAGACCTCCGACAAATGTTTGGCCAAATTTGGTAAATATTAG	382
Db	1016	CCCTCCGGTTCAGGGACCCCGACTTGGGGCAAAATGTTGGGGCAATTCGGAAAAATTTTAG	1075
QY	383	ATGTTGAAATATTATTTTAAATGACCGGGGCTCGAAGGGAATTTGGTTCGTAATTTCGAA	442
Db	1076	ACGGGAATATATTTTAAACAGACCGGGGCTCCAAAGGTTTGGGTTTGTAACTTTGAAA	1135
QY	443	ATTAGCGCGATGCCGACAGGGCGAGGAGAAATTGACAGGTAACGCTGTAGAGGGCCGTA	502
Db	1136	CTTAGCTACGATGCTGACCCGAGCCCGGAGAAAGCTTAATGGGACGATCGTAAAGGACCGA	1195
QY	503	AAATCGAGGTTAATTAATGCGACAGCACGCGTAGTAGCTTAATTAAGAAAGCCGTGAACCCCT	562
Db	1196	AAATTTAGAGTCAATTAATGCGACAGCGCCGAGTGAATCAACAAGAAAGCGGGAAACCCCT	1255
QY	563	ACACCAATGCGCTGGAATTAATCAAGTTGTGGGCGCGGTCTACAGCCCGCATTTCTATG	622
Db	1256	ACACCAACGCGCTGGAAAGCTAAATCAGAGGTTCGCGCAGACTTACCGGCGCTGAATTCATG	1315
QY	623	CAGGACAGGTCGTGTGTGCCAGGCAAC	651
Db	1316	CAGTACCGGGTTCCTTACCCCATCAC	1344

RESULT 6
US-09-664-761-11804
Sequence 11804, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Neomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263.6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669

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1  PRIOR FILING DATE: 2001-01-30
2  PRIOR APPLICATION NUMBER: PCT/US01/00665
3  PRIOR FILING DATE: 2001-01-30
4  PRIOR APPLICATION NUMBER: PCT/US01/00668
5  PRIOR FILING DATE: 2001-01-30
6  PRIOR APPLICATION NUMBER: PCT/US01/00663
7  PRIOR FILING DATE: 2001-01-30
8  PRIOR APPLICATION NUMBER: PCT/US01/00662
9  PRIOR FILING DATE: 2001-01-30
10 PRIOR APPLICATION NUMBER: PCT/US01/00661
11 PRIOR FILING DATE: 2001-01-30
12 PRIOR APPLICATION NUMBER: PCT/US01/00670
13 PRIOR FILING DATE: 2001-01-30
14 PRIOR APPLICATION NUMBER: US 60/234,687
15 PRIOR FILING DATE: 2000-09-21
16 PRIOR APPLICATION NUMBER: US 09/608,408
17 PRIOR FILING DATE: 2000-06-30
18 PRIOR APPLICATION NUMBER: US 09/774,203
19 PRIOR FILING DATE: 2001-01-29
20 NUMBER OF SEQ ID NOS: 49117
21 SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
22 SEQ ID NO 11804
23 LENGTH: 473
24 TYPE: DNA
25 ORGANISM: Homo sapiens
26 FEATURE:
27 OTHER INFORMATION: MAP TO AC006075.1
28 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.67
29 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
30 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.48
31 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.5
32 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.57
33 US-09-864-761-11804

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	Query Match	Best Local Similarity	9.2% 1.6%	Score 123.8	DB 9	Length 473
	Matches 131	Conservative	0	Mismatches 12	Indels 0	Gaps 0
QY	220	CAGACAGATGATGCGCCCGACCGACGCGCCAGCCGACAGACACAACCTTCTGAAAAACA	279			
Db	269	CAGACAGATGACGAGACCGACCGAGATGCGCCGACCAACAACCTTCTGAAAAACA	328			
QY	280	GAAGAACAGTCCAGGCCCAAGCGCGTGCATGTGTCCAAATCCCTTCGGTTCCGGGAT	339			
Db	329	GAAGAACAGTCTCAGCCCAAGCGCGTGCATGTGTCCAAATATCCCTTCAGGTTCCGGGAT	388			
QY	340	CCAGACTCCGACCAATGTTTG	362			
Db	389	CCGACTCCAGACCAATGTTTG	411			

RESULT 7
 US-09-864-761-28375
 Sequence 28375, Application US/09864761
 Patent No. US20020048763A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David R.
 APPLICANT: Hanzel, David K.
 APPLICANT: Chen, Wensheng
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: Aecm1ca-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 CURRENT FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/532,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263.6
 PRIOR FILING DATE: 2000-10-04


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QY 1 GCGGCGCCCTGACACATAGCTCAG-CTTATGCTCAGCGAGTTGCTCCAGCCCGAG 59
DB 134 GCGGCTGCCCCCTGACACATAGCTCAGCTTACGCTTCCGCGGAGTTGCTCCCGCAG 193
QY 60 AATGGCATCTCT-GCAGAAATACAGCGCCCTCATCCCATCCCGCGCCAGAG-ACACCGGC 117
DB 194 AAGCGATATCCCGGGAATACAGCGCCCTCATCCCATCCCGCGGCGAGGTACACAGGC 253
QY 118 CAGCCCACTGCTCCCGC-CCACACATTAACCTTG-ATCCTCTACACAGACGACTCGAG 175
DB 254 CAGACACGAGTTCCCGAGACACATTAACCTGTAACCTTCCCGCCAGACGACTCGAG 313
QY 176 CAGAGC---GCTTATACAGCGCAG-CCGTCTCCGCGACCGCCACA 219
DB 314 CAGAGCCCGGCGAGACAGAGCGGTGACAGCCGTCTCTGGACCGCCACA 361

RESULT 10
US-09-864-761-22653
; Sequence 22653, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 22653
; LENGTH: 224
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; OTHER INFORMATION: MAP TO AC006075.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
; OTHER INFORMATION: NT HIT: g18922072, EVALUATE 1.00e-123
; OTHER INFORMATION: SWISSPROT HIT: Q09457, EVALUATE 8.00e-03
; OTHER INFORMATION: EST_HUMAN HIT: A0118435.1, EVALUATE 1.00e-123
US-09-864-761-22653

Query Match 6.6%; Score 88; DB 9; Length 224;
Best Local Similarity 82.6%; Pred. No. 1.4e-14;
Matches 185; Conservative 0; Mismatches 30; Indels 9; Gaps 7;

QY 5 CCGCCCTGACACATAGCTCAG-CTTATGCTCAGCGAGTTGCTCCAGCCCGAGATG 63
DB 1 CTGCCCCCTGACACATAGCTCAGCTTACGCTTCCGCGGAGTTGCTCCCGCAGAGC 60
QY 64 GCATCTCT-GCAGAAATACAGCGCCCTCATCCCATCCCGCGCCAGAG-ACACCGCGCAGC 121
DB 61 GATCCCCCGGGAATACAGCGCCCTCATCCCATCCCGCGCCAGAGTACACAGCGCCAGA 120
QY 122 CCAGTGTCCCGC-CCACACATTAACCTTG-ATCCTCTACACAGACGACTCGAGCAGA 179
DB 121 CCACGGTTCCTGAGACACATTAACCTGTACTCTCCCGCCAGAGCAGACTCTCGAGCAGA 180
QY 180 GC---GCTTATACAGCGCAG-CCGTCTCCGCGACCGCCACA 219
DB 181 GCGCCGCGAGACAGAGCGCTCAGAGCCGTCTCTGGACCGCCACA 224

RESULT 11
US-09-864-761-5893
; Sequence 5893, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663

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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 5893
LENGTH: 454
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006075.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.9
US-09-864-761-5893

Query Match 6.4%; Score 86.4; DB 9; Length 454;
Best Local Similarity 83.5%; Pred. No. 6e-14;
Matches 157; Conservative 0; Mismatches 26; Indels 5; Gaps 5;

QY 1 GCGGCGCGCCCTGACACATGCTCTGAG-CTTATGCTCTGAGCGCAGTTGCTCCACCCGAG 59
DB 246 GCGGCTGCTGACACATGCTCTGAGCGCAGTTGCTCCACCCGAG 305
QY 60 AATGAGCATCTCT-GCAGAAATACACGCGCCCTCATCCCATCCGCGCCAGAG-AACCGGGC 117
DB 306 AACGCTATCCCGGGAATACACGCGCCCTCATCCCATCCCGCCAGAGTACACAGGCG 365
QY 118 CAGCCCACTGTCCTCCG-CACACATTAACCTTG-ATCCTCTTACACAGACGCACTCGGAG 175
DB 366 CAGACCACTGTCCTCCG-CACACATTAACCTTG-ATCCTCTTACACAGACGCACTCGGAG 425
QY 176 CAGAGCGC 183
DB 426 CAGAGCGC 433

RESULT 12
US-10-292-798-1837/c
Sequence 1837, Application US/10292798
Publication No. US2003023583A1
GENERAL INFORMATION:
APPLICANT: SUMA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABRATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1837
LENGTH: 2350

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
LOCATION: source
FEATURE:
LOCATION: (1)..(2350)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(2150)
FEATURE:
NAME/KEY: modified_base
LOCATION: (2)..(2)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (7)..(7)
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FEATURE:
NAME/KEY: modified_base
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NAME/KEY: modified_base
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NAME/KEY: modified_base
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NAME/KEY: modified_base
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FEATURE:
NAME/KEY: modified base
LOCATION: (179)..(179)
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FEATURE:
NAME/KEY: modified base
LOCATION: (195)..(195)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (197)..(197)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (209)..(209)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (212)..(212)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (214)..(214)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (216)..(216)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:

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NAME/KEY: modified base
LOCATION: (218)..(218)
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FEATURE:
NAME/KEY: modified base
LOCATION: (290)..(291)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
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OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (309)..(309)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (315)..(315)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (317)..(317)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (320)..(320)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (323)..(323)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified base
LOCATION: (327)..(327)
OTHER INFORMATION: a, t, c, g, unknown or other

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Query Match 4.3%; Score 58; DB 12; Length 2350;
 Best Local Similarity 57.5%; Pred. No. 1.8e-05;
 Matches 103; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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QY 1140 ATATTAAATGATTAACCACTTAAACAACAGCAAAAAACAACAAACAAATTAAC 1199
DB 1120 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1061
QY 1200 AACCTTCAATGCGGAGAGAGAAAGCTTCCGAGCCCGAGTGCGACATGCGAG 1259
DB 1060 AAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1001
QY 1260 TAGACATCATCTTTAGCACTCAAGAAAAACAAGAAAAAATTAATTA 1318
DB 1000 AGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942

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RESULT 13
US-10-017-161-2191/c
; Sequence 2191, Application US/10017161
; Publication No. US2003014368A1
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABURATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 08435/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; PRIOR FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2191
; LENGTH: 2350
; TYPE: DNA

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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: source
LOCATION: (1)..(2350)
FEATURE:
NAME/KEY: CDS
LOCATION: (201)..(2150)
FEATURE:
NAME/KEY: modified_base
LOCATION: (2)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (7)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (9)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (13)..(15)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (17)..(18)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (20)..(21)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (23)..(24)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (31)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (34)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (39)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (41)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (49)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (51)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (71)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (73)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (77)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base

LOCATION: (85)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (90)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (92)..(93)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (95)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (99)..(100)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (103)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (106)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (109)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (111)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (113)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (170)..(171)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (179)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (195)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (197)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (209)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (212)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (214)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (216)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (218)

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OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (290)-(291)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (302)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (309)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (317)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (320)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (323)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (327)
OTHER INFORMATION: a, t, c, g, unknown or other
FEATURE:
NAME/KEY: modified_base
LOCATION: (332)

Query Match
Best Local Similarity 57.5%; Score 58; DB 13; Length 2350;
Matches 103; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

QY 1140 ATATTAAATGATTAACCACTTAACCAACGCAAAACCAAAACCAAAACCAAAACCC 1199
DB 1120 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1061
QY 1200 AACCTTCATGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1259
DB 1060 AAAAAAAAAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1001
QY 1260 TAGGACATCATCTTAGCAACTCAAGAAACGCAAAAAAAAAAAAAAAAAAAAAATTA 1318
DB 1000 AGGGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 942

RESULT 14
US-09-908-975-27923
Sequence 27923, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: FRIGER, Shimon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
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NUMBER OF SEQ ID NOS: 32337
SOFTWARE: Patent version 3.0
SEQ ID NO 27923
LENGTH: 65
TYPE: DNA
ORGANISM: Mus musculus
US-09-908-975-27923
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Query Match
Best Local Similarity 92.3%; Score 57; DB 13; Length 65;
Matches 60; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 1226 GCTTCCGAGCCCGAGTGTGCGACACATGACATGAGCACTTATGACAACTCAAG 1285
DB 1 GCTTCCGAGCCCGAGTGTGCGACATGACATGAGCACTATGTTAGCAACTCAAG 60
QY 1286 AAACA 1290
DB 61 AAACA 65
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RESULT 15
US-10-311-455-1669/c
Sequence 1669, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIRENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determini
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: PCT/EP01/07537
PRIOR FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1669
LENGTH: 6668
TYPE: DNA
ORGANISM: Artificial Sequence
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KEY: unsure
LOCATION: 4733
OTHER INFORMATION: n is a or g or c or t
US-10-311-455-1669
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Query Match
Best Local Similarity 57.0%; Score 55.8; DB 13; Length 6668;
Matches 102; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
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QY 1140 ATATTAAATGATTAACCACTTAACCAACGCAAAACCAAAACCAAAACCAAAACCC 1199
DB 5716 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5657
QY 1200 AACCTTCATGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1259
DB 5656 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5597
QY 1260 TAGGACATCATCTTAGCAACTCAAGAAACGCAAAAAAAAAAAAAAAAAAAAAATTA 1318
DB 5596 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5538
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Search completed: January 15, 2004, 06:53:14
Job time : 2630 secs

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OY	352	CAAAATGTTGGCCAAATTTGGTAAATAATTTAATGTTGAATTTATTTTAAATGACGGGGC	411
Db	1389	CAAAATGTTGGTCAATTTGGTAAATCTTAAGATGTTGAATTTATTTTAAATGACGAGGC	1448
OY	412	TCGAAGGGAATTTGGTTCGTACTTTCGAAATAATGTGCGAATGCGACGAGGCGAGGAG	471
Db	1449	TCAAAGGGAATTTGGTTCGTAACTTTCGAAATAATGTGCGAATGCGAGCGAGGCGAGGAG	1508
OY	472	AAATTCGACGGTACCGGTGTAGAGGGCCGTAAATTCAGAGTTAATATGACACGACGCG	531
Db	1509	AAATTCACGGGACCGGTGTAGAGGGCCGTAAATTCAGAGTTAATATGACACGACGCT	1568
OY	532	GTGATGACATAATAAAAGGCGGTGAACCCCTACACCAATGCGTGGAAATTTAAATCCAGTT	591
Db	1569	GTAATGACAAATTAATAAAGACCGTCAACCCCTATTAATAATGGCTGGAAATTAATCCAGTT	1628
OY	592	GTGGGCGCGGTCTACAGCCGCCGACTTATACAGAGGACGAGTGCTGTGTGTCAGGCGCAC	651
Db	1629	GTGGGTGACGTACGTACAGTCCGGAATTTATATCAGAGGACGAGTGCTGTGTGTCAGGCGCAC	1688
OY	652	CAGAGAGGATCTTCATCATGTATCAGAGGGCCCGAGTTCACTGTATATATCTTCGCAATGCGT	711
Db	1689	CAGAGAGGATCTTCATCATGTATCAGAGGGCCCGAGTTCACTGTATATATCTTCGCAATGCGC	1748
OY	712	GGCTTTCCATATCCGGGCGGCACACTGCTGACAGCTGATACCGAGGGGCTCACTTCGAGGC	771
Db	1749	GGCTTCCCGTATCCAGAGGACGACCGGCGGCGGCGCTACCGAGGGGCGCACCTCGAGGC	1808
OY	772	CGTGTGCGACCGGTGTACACACTTCAGAGCTGTGGGCGCCCACTCCCAATCCGGGC	831
Db	1809	CGCGGTCCGACCGGTGTACACACTTCAGAGGCGGCGGCGCCCGCCCGCCCATCCGGGC	1868
OY	832	TATGGCGGAGTAGTATCAAGAGCGAGTGTATGGCAATAATGTCTACAGGGTGTAC	891
Db	1869	TACGGCGGTGTGTATTACC--CAGAGTGAATTTATAGTGTACAGACATTTATAGTGTAT	1926
OY	892	GCTGATATCCGCTACGCCAGCCCACTCCCTGCACCTGTGCTGCTACAGTGA-----	944
Db	1927	GCTGATATCCGCTACGCCAGGCTACCCCTGCACCTGCGCTGCTACAGTGAAGAAAT	1986
OY	945	-----CAGTTACGGAGCGAG	958
Db	1987	CAGTTCCGTCCTTCGTTGACAGAGATGAATTTCTTGTAACACTCTGCAAGTTACGGAGCGAG	2046
OY	959	TTTATGCTGCGGACCCCTTACCAACCACTATGCTCCAGCCGCCCACTACGCGCTTGGTG	1018
Db	2047	TTTATGCTGCGGACCCCTTACCAACCACTATGCTCCAGCCGCCCACTACGCGCTTGGTG	2106
OY	1019	CCATGAATGCTTTTTCGCGCCCTTGACCGATGCCAAGACTAGAGAGCCATGTATATGTGG	1078
Db	2107	CCATGAATGCTTTTTCGACCTTTGACCTGTATGCTGATGCTAGATGATGTGG	2166
OY	1079	GTTCTGTTCTTTCTTCACTTATGACAGGTATATATACCAAGGGGGATATACAACGTTTGGTC	1138
Db	2167	GTTCTGTTCTTTCTTCACTTATGACAGGTATATATACCGAGGGGGATATACAACGTTTGGTC	2226
OY	1139	CATATTAATATATTAACCATTTAAACAACAAGCAAAAAACAACAAAAACAACAAAAAAC	1198
Db	2227	CATATTAATATATTAACCATTTAA-----	2250
OY	1199	CAACCTTCCAAATGTGGGAGAGAGAGACCTTTCCGAGGCCGAGTGTTCGACACATGCA	1258
Db	2251	-AACCTTCCAAATGTGGGAGAGAGAGACCTTTCCGAGGCCGAGTGTTCGACACATGCA	2309
OY	1259	GTAGACATTCACCTTAGACACTCAAGAAGAAACAAGAAAAAAGAAAAAAGAAAAAATTA	1318
Db	2310	GTAGACATTCACCTTAGACATTTTAAAAAAGAAAAAATTAACAAGAAAAAAGAAAAAATTA	2368

RESULT 2
US-09-176-657-5
; Sequence 5, Application US/09176657

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; Patent No.6020164
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/176,657
; CURRENT FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-09-176-657-5

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Query Match	Similarity	20.6%	Score 275.6	DB 3	Length 1506
Match	Local Similarity	60.2%	Pred. No. 1.5e-68	DB 3	Length 1506
Matches	Conservative	0	Mismatches 354	Indels 43	Gaps 7
QY	222	GACAGATGATGCGCGCCCGACCGACCGCGCAGC--CCAGACACMACCTTCTGAAACAC	278		
Db	452	GACAGAGGTGAGACACAGACAGCGCCAGCAGCTACAGACACAAAGTAGTGAATTC	511		
QY	279	AGAAAACAGTCCCAAGCCCAAGCGGCTGCAATGTGTCCAAATCCCCCTTCCGGTTCGGGA	338		
Db	512	AGAAAGTAATCTACCCCGAAACGGCTGCATGTCTCAAAATTCCTTCCGCTTCGGGA	571		
QY	339	TCCAGACCTCCGACAAATGTTTGGCCAAATTTGTGTAATAATTAAGTGTGAATTAATTTT	398		
Db	572	CCCTGACCTCCGAGAGATGTTTGGCAGATTGGCAAAATCCTAGATGTAAGAAATATCTT	631		
QY	399	TAAATGACGGGGCTCGAAGGGATTTGGTTTCGTACTTTGCAAAATAGTGGATTCGGA	458		
Db	632	TAAATGAAGTGGCTCTAAGGGATTCGGGTTCTGTAACTTTGCAAGATAGTGTGATGAGA	691		
QY	459	CAGGCGGAGGAGAAATTTGCACGGTACCCTGTGTGAGGGCCGTAAATTCAGAGTTAATA	518		
Db	692	CAGGCGGAGGAGAAATTTGCACGGCACCGTGTGAGAGGGCGTAATAATTCAGAGTTAATA	751		
QY	-519	TGCGACAGCAGCGGTGATGACTAATTAATAAAGGCGGTGAACCCCTACACCAATGCTGGAA	578		
Db	752	TGCTACAGCAGCTGTAATGACCAATTAAGAGATGTCAACACATATGCAATGCTTGGAA	811		
QY	579	ATTAAATTCAGATTGTGGCGCGGATCTACAGCCCGACCTCTTATGACG-----GCA	628		
Db	812	ATTAAAGCCAGTATGTTGGAGCTGATATATGGTCCGAGTATATACAGATCCAGCTTTCA	871		
QY	629	CGTGTGCTTGTGCGAGGCGCAACAGAGAGGATTTTCATGTA--CAGTGGCCCCAGTTC	686		
Db	872	AGCAGATGTGTCCCTTAGGCAATGATGACGACGTCGCCCTTACAGAAAGAGGGGGTATCAA	931		
QY	687	ACTGTATATATCTCTGCAATGCTGTGGCTTCAATA--TCGGCGCGCACTGTGTCAGC	743		
Db	932	CACTTACATCTCTTAAATCAATCTCTGCTTCCCTTACCTACTGACGACACACAGGACG	991		
QY	744	TGCATATCCGAGGGGCTCACTTCGAGGCGGTGTGCGACCGGTGTACAACATTTCAAGC	803		
Db	992	CGCTTTAGAGAGAGCCATTTGAGGGGAGAGGGCGGACAGTATATGGGTGAGTCCGA--	1049		
QY	804	TGCGCGCGCCCAACCCCAATCCCGGCTATAGGGGAGTATGTATCAAGAGCCAGTCTA	863		
Db	1050	-GCGTACTCTCAACAGCCATCCCGCTTATCCAGGGGTGATATGACGCTTAAG----	1104		
QY	864	TGCGCAATAAATTTGCTACAGGGGTGTTACGCTGCATACCGCTACGCCAGCCACCCCTGC	923		
Db	1105	-----ATTGACACAGCCTGCTACTCTGCAACCGCAGCCACCGCTGCTGCAGC	1149		

QY	924	CACGCTGCTCCCTACAGTGA	CAGTTACGGA	CGAGTTATGCTGGCCGACCCCTACACCA	983
	1150	CGCTGCACGCCCTTACAGTGA <td>CGGTTAAGCAGGGGTGACACAGCCGACCCCTTACATGC</td> <td>1209</td> <td></td>	CGGTTAAGCAGGGGTGACACAGCCGACCCCTTACATGC	1209	
QY	984	CACACTTGCTCCAGCCCCCACTTACGGCGTGTGGTCATGATGCTTTTGGCGCCCTTGAC	1043		
Db	1210	C---CTTGGCCCTCCGCTACGCTATGAGAGTTGGCGCTGTGGCGAGTTATATCCAGAGTGG	1266		
QY	1044	CGATGCCAAGCTACGAGCCGATGCTGAATGATGTGGGTGCTGTATCTTCTTCAATTGCAGGC	1103		
Db	1267	CTACAGCCGATTTGGCCCCCTTACTGAAGTGA <td>CGTGAACCCCTGCATAATGGACAGCCCC</td> <td>1328</td> <td></td>	CGTGAACCCCTGCATAATGGACAGCCCC	1328	
QY	1104	TAGTATATACCAAGGGGGATCAACCCGTTTTGCTTCATATTTAAATGATTAACAATTAA	1163		
Db	1327	CAGTTTCATGAGGCCCTGCGCTATTTGCAATATTACTAGTAGAGAACTATAGCAAGATGA	1386		
QY	1164	CAACCAAGCAAAAAACAACAAAAACAACAAAAACCA	1201		
Db	1387	AGAGAAAAACAACAAACAACAACAACAACAACA	1424		

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RESULT 3
US-09-421-299-5
: Sequence 5, Application US/09421299
: Patent No. 6524579
: GENERAL INFORMATION:
: APPLICANT: Bandman, Olga
: APPLICANT: Tang, Y. Tom
: APPLICANT: Corley, Neil C.
: APPLICANT: Guegler, Karl J.
: APPLICANT: Lu, Aina
: APPLICANT: Baughn, Mariah R.
: TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
: FILE REFERENCE: PF-0611 US
: CURRENT APPLICATION NUMBER: US/09/421,299
: CURRENT FILING DATE: 1999-10-20
: EARLIER APPLICATION NUMBER: 09/176,657
: EARLIER FILING DATE: 1998-10-21
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: PERL Program
: SEQ ID NO 5
: LENGTH: 1506
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE: -
: OTHER INFORMATION: 1250374
: US-09-421-299-5

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Query Match	20.6%	Score 275.6	DB 4	Length 1506	
Best Local Similarity	60.2%	Pred. No. 1.5e-68			
Matches	601	Conservative	0	Mismatches 354	Indels 43
				Gaps	7
QY	222	GACAGATGATCCGCCCGGACCGAGGGCCAGC	---	CCGAGACACACTTCTGAAAAAC	278
Db	452	GACGAAAGGTGAGACACAGACAGACGGCACAAGTGCACAGACACAAAGTATGAAAAATTC			511
QY	279	AGAAACAAAGTCCGACGCCAGCGGCTCATGTGTCCAACATCCCTTCGGTTCGGGA			338
Db	512	AGAGAGTAAATCTACCCGGAACGGCTGCATGTCTTAATATTCCTTCCTTCGGCTTCGGGA			571
QY	339	TCCAGACTCCGACAAATGTTTGGCCAAATTTGGTAAATATTAGATGTTGAAATTATTTT			398
Db	572	CCCGACCTCCGGACAGATGTTTGGCAGATTTGGCAAAATCCTAGATGTAAGAAATATATCTT			631
QY	399	TAAAGCGGGGCTCGAAGGATTTGGTTGTCTTAATCTTCGAAAAATAGTGGGATGCGGA			458
Db	632	TAAATGAAGTGGCTCTAAGGATTTGGGTTGGTAACTTTCGAAATATAGTGATGACGA			691
QY	459	CAGGGCCAGGAGAAATTGCACGATCCTGTGTAAAGGCGGTAAATCCGAGTTAAATA			518
Db	692	CAGGGCCAGGAGAAATTACACGCAACCTGTGTAAAGGCGGTAAATCCGAGTTAAATA			751

[illegible]

RESULT 4
 US-09-014-969-14
 Sequence 14, Application US/09014969
 Patent No. 5965397
 GENERAL INFORMATION:
 APPLICANT: Jacobs, Kenneth
 APPLICANT: McCoy, John M.
 APPLICANT: Lavallie, Edward R.
 APPLICANT: Racle, Lisa A.
 APPLICANT: Metberg, David
 APPLICANT: Treacy, Maurice
 APPLICANT: Spaulding, Vikki
 APPLICANT: Agostino, Michael J.
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
 TITLE OF INVENTION: ENCODING THEM
 NUMBER OF SEQUENCES: 32
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02140
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-014-969-14

Query Match 3.8%; Score 51.4; DB 2; Length 2447;
Best Local Similarity 52.1%; Pred. No. 0.00015;
Matches 112; Conservative 1; Mismatches 102; Indels 0; Gaps 0;

QY 1104 TAGATATACCAAGGGGATACACCGTTTGTCTCCATATTAATGATTAACCATTA 1163
DB 2209 TTGACTTTAAATGTGCAATTAACCTTTGGAGAAAAAABAAAAA 2268
QY 1164 CAACAACGAAAAAACAACAAAAAACAACCTTCCATGTGGGAGAGAG 1223
DB 2269 AA 2328
QY 1224 AAGCTTCCGAGCCGAGTGTCCGACATGAGTGAATCACTTACCACTCA 1283
DB 2329 AA 2388
QY 1284 AGAACAACGAAAAAACAACAAAAAACAACCTTCCATGTGGGAGAGAG 1318
DB 2389 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 2423

RESULT 5

US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: PALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOXLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:

APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-Fis
US-08-232-463-14

Query Match 3.7%; Score 50; DB 1; Length 7218;
Best Local Similarity 7.5%; Pred. No. 0.0007;
Matches 17; Conservative 132; Mismatches 77; Indels 0; Gaps 0;

QY 1106 GTTATACCAAGGGGATACACCGTTTGTCTCCATATTAATGATTAACCATTA 1165
DB 1467 GCAAGTAGTTAAAGATAGAAATTTGTACRRRRRRRRRRRRRRRRRRRR 1408
QY 1166 AACAGCAAAAAACAACAAAAAACAACCTTCAATGTGGGAGAGAGAA 1225
DB 1407 RRR 1348
QY 1226 GCTTCCGAGCCGAGTGTTCGACATGACGTAGACATCATCTTAGCAACTCAAG 1285
DB 1347 RRR 1288
QY 1286 AAACAACGAAAAAACAACAAAAAACAACCTTCCATGTGGGAGAGAG 1331
DB 1287 RRR 1242

RESULT 6

US-08-628-417-6
Sequence 6, Application US/08628417
Patent No. 5627054
GENERAL INFORMATION:
APPLICANT: GILLESPIE, DAVID
TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
TITLE OF INVENTION: POLYMERASE CHAIN REACTION
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
ADDRESSEE: DEFENSE COMMAND
STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
CITY: ABERDEEN PROVING GROUND
STATE: MARYLAND
COUNTRY: USA
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,417
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BIFFONI, ULYSSES J
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 398-94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158

TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligodeoxynucleotide
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
US-08-628-417-6

Query Match 3.7%; Score 49; DB 1; Length 240;
Best Local Similarity 53.4%; Pred. No. 0.00019;
Matches 103; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1126 AACCGTTTGTCTCATTTAAATGATTAACCTTAACCAACAGCAAAACAAACAA 1185
DB 28 AATTAATTTTACTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT 87
QY 1186 AAAAAAACAACCACTTCCATGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1245
DB 88 AAAAAAACAACCACTTCCATGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 147
QY 1246 TCGGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 1305
DB 148 AAAAAAACAACCACTTCCATGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207
QY 1306 AAAAAAACAATTA 1318
DB 208 AAAAAAACAATTA 220

RESULT 7

US-09-835-811-1
; Sequence 1, Application US/09835811
; Patent No. 6482936
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; FILE REFERENCE: CL0012228
; CURRENT APPLICATION NUMBER: US/09/835,811
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 1696
; TYPE: DNA
; ORGANISM: Human
US-09-835-811-1

Query Match 3.6%; Score 48; DB 4; Length 1696;
Best Local Similarity 53.1%; Pred. No. 0.0011;
Matches 102; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1127 ACCGTTTGTCTCATTTAAATGATTAACCTTAACCAACAGCAAAACAAACAA 1186
DB 1502 ACTGATAGATTTAAAAAATTTTAAAAAATTTTAAAAAATTTTAAAAAATTTT 1561
QY 1187 AAAAAAACAACCACTTCCATGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1246
DB 1562 AAAAAAACAACCACTTCCATGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1621
QY 1247 GCGACATGACATGACATGACATGACATGACATGACATGACATGACATGACAT 1306
DB 1622 AAAAAAACAACCACTTCCATGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1681
QY 1307 AAAAAAACAATTA 1318
DB 1682 AAAAAAACAATTA 1693

RESULT 8

US-09-027-064-3
; Sequence 3, Application US/09027064
; Patent No. 6133006
; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; APPLICANT: BERGMA, DERR
; TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,064
; FILING DATE: 20-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,924
; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1338 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-027-064-3

Query Match 3.4%; Score 45.2; DB 3; Length 1338;
Best Local Similarity 47.8%; Pred. No. 0.0062;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 3 GGGCCGCTGACACATGAGCTGACCTTATGCTTACAGCGCAATTTGGCTCCACCCAGAT 62
DB 686 GGTCTGCTCCCATCACCACCCCTTACCCACCCCGAGAGCTATGATGAGCTGTG 745
QY 63 GGCATCTGACAGATACAGCGCCCTCATCCCATCCGCGCAGAGACAGCGCCAGCGC 122
DB 746 GGGCGCTGCTACTGCTCTCCCATCTCAGCGCTGCCCCCAGACACCGGCTGCT 805
QY 123 CACTGCTCCCGCAGACATTAATTTGATCTCTTACACAGACGATCTGAGACAGAGCG 182
DB 806 CAGCCCTCGGAGCTGAGATGACTGAGAGTGTCTCACCCCTCCGCTCTGATGACCTG 865
QY 183 CTATTAACAGCCGACAGCGCTCTCCGCGACCGCCACAGACAGATGATGAGCCGCCGAGC 242
DB 866 CCACTCTGGGGCTTCACTCTGCGCTCTGAGTATCCCAAGACAGACAGCAAGCTGTG 925
QY 243 CGAGGCGAGCCCGCAGACCACTTCTGAATAC 276
DB 926 ACCCTGCCCCCTCTCTGGGGCCCTCTCTGAATAC 959

RESULT 9

US-09-271-815-3
; Sequence 3, Application US/09271815
; Patent No. 6297036
; GENERAL INFORMATION:
; APPLICANT: BERGSM, DERK
; TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE PROTEIN KINASE-HTLAR33
; FILE REFERENCE: GH-70172-1
; CURRENT APPLICATION NUMBER: US/09/271,815
; EARLIER FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: 09/027,064
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 60/053,924
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1338
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-271-815-3

Query Match 3.4%; Score 45.2; DB 3; Length 1338;
Best Local Similarity 47.8%; Pred. No. 0.0062;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 3 GGGCCGCTGACACATGCTAGCTTATGCTCAGCGCAGTTGCTCCACCCAGAAAT 62
DB 686 GGTGTCTCCATCAACACCTTCAACACACCCCGAGCTGATGATGAGCTGTGTG 745
QY 63 GGCATCTGACAAATACAGCGCCCTCATCCCATCCCGCGCAGAGACACCGCCAGCC 122
DB 746 GGGCGCTGTGACTGTCTCCCACTCAACGAGCGCTGCCCCCAGACACCGGCTGCT 805
QY 123 CACTGTCCCGCCACACATTTAACTTATCTCTTAACAGACGACATCTCGAGAGAGCG 182
DB 123 CACTGTCCCGCCACACATTTAACTTATCTCTTAACAGACGACATCTCGAGAGAGCG 182
QY 806 CAGCCCTCGAGCTGAGTGTGAGAGTGTCTCAACCTCTCCCTCTGATGACCTTG 865
DB 183 CTATACAGAGCGACAGCGCTCTCCGACCGCCACACAGACAGATGATGCGCCCGAC 242
QY 866 CCACTGTGGGCTCACTGCTGCTCCGTGTGTATCCCAAGACACAGACGACACTGTG 925
QY 243 CGAGCGCCAGCGCCGACACACACCTTGTGAAAC 276
DB 926 ACCCTGCCCCCTCCCTGAGGCGCCCTCTGAAAGC 959

RESULT 10
US-09-027-064-1
; Sequence 1, Application US/09027064
; Patent No. 6133006

; GENERAL INFORMATION:
; APPLICANT: SHABON, USMAN
; TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE
; TITLE OF INVENTION: PROTEIN KINASE-HTLAR33
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAITNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; APPLICATION NUMBER: US/09/027,064
; FILING DATE: 20-FEB-1998
; CLASSIFICATION:

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,924
; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70172
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2394 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-027-064-1

Query Match 3.4%; Score 45.2; DB 3; Length 2394;
Best Local Similarity 47.8%; Pred. No. 0.0087;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 3 GGGCCGCTGACACATGCTAGCTTATGCTCAGCGCAGTTGCTCCACCCAGAAAT 62
DB 1742 GGTGTCTCCATCAACACCTTCAACACACCCCGAGCTGATGATGAGCTGTGTG 1801
QY 63 GGCATCTGACAAATACAGCGCCCTCATCCCATCCCGCGCAGAGACACCGCCAGCC 122
DB 1802 GGGCGCTGTGACTGTCTCCCACTCAACGAGCTGCCCCCAGACACCGGCTGCT 1861
QY 123 CACTGTCCCGCCACACATTTAACTTATCTCTTAACAGACGACATCTCGAGAGAGCG 182
DB 1862 CAGCCCTCGAGCTGAGTGTGAGAGTGTCTCAACCCCTCCGCTCTGATGACCTG 1921
QY 183 CTATACAGAGCGACAGCGCTCTCCGACCGCCACACAGACAGATGATGCGCCCGAC 242
DB 1922 CCACTGTGGGCTCACTGCTGCTCCGTGTGTATCCCAAGACACAGACGACGCTGTG 1981
QY 243 CGAGCGCCAGCGCCGACACACACCTTGTGAAAC 276
DB 1982 ACCCTGCCCCCTCCCTGAGGCGCCCTCTGAAAGC 2015

RESULT 11
US-09-271-815-1
; Sequence 1, Application US/09271815
; Patent No. 6297036

; GENERAL INFORMATION:
; APPLICANT: BERGSM, DERK
; APPLICANT: SHABON, USMAN
; TITLE OF INVENTION: A YAK-1 RELATED SERINE/THREONINE PROTEIN KINASE-HTLAR33
; FILE REFERENCE: GH-70172-1
; CURRENT APPLICATION NUMBER: US/09/271,815
; EARLIER FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: 09/027,064
; EARLIER FILING DATE: 1998-02-20
; EARLIER APPLICATION NUMBER: 60/053,924
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2394
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-271-815-1

Query Match 3.4%; Score 45.2; DB 3; Length 2394;
Best Local Similarity 47.8%; Pred. No. 0.0087;
Matches 131; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

QY 3 GGGCCGCTGACACATGCTAGCTTATGCTCAGCGCAGTTGCTCCACCCAGAAAT 62

Db 1742 GGGTCGTCCCATCAACCAACCTCAACCAACCCCGAGCTGATGTGAGCTGTG 1801
Qy 63 GGCATCTCGAGATATACAGGCGCCCTCATCCCATCCCGGCGAGACACCGGCGAGC 122
Db 1802 GGGGCGCTGTGACTGTCTCCCACTCAACCAAGCGCTGCGCCCGACACCGGCTGCT 1861
Qy 123 CACTGTCCCGGCGACATTAATCTTGATCTCTCAACAGAGCACTCGAGCAGAGCG 182
Db 1862 CAGCGCTCGGAGCTCGGATACAGAGGTGTCTCAACCCCTCCGCTCTGATGACCTG 1921
Qy 183 CTTATATACAGCGACAGCGCTCTCCGACCCGACACAGACAGATGATCGGCGCGAC 242
Db 1922 CCATCTGGGGGCTCACTGCGCTCCGCTGTATACCCAGAGACAGACAGCTGTG 1981
Qy 243 CGAGCGCGAGCGCCGACAGACACACCTTCTGAAC 276
Db 1982 ACCCTGCCCCCTCCCTGCGGCGCCCTCTCTGAACG 2015

RESULT 12

US-08-676-967-2
Sequence 2, Application US/08676967
Patent No. 5747317
GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,967
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-676-967-2

Query Match 3.4%; Score 45; DB 1; Length 2277;

Best Local Similarity 32.4%; Pred. No. 0.0096;
Matches 109; Conservative 46; Mismatches 178; Indels 3; Gaps 1;

Qy 215 CCACACAGACAGATATGTCGCGCCCGACGAGCGCCGACGACCAACCTTCTGA 274
Db 257 CNAAGARARAGGNAARAAAGAAAYWSNGARTGVCNABARARAGCCNABARAG 316
Qy 275 ACACAGAAAACAAGTCCGACGCGCAAGCGGTGATGTCTCAATCCCTTCGGTTC 334
Db 317 ARCCNABRGTCNGAFAAARABGACNMGNTYNAATHMGNAAYTNWSTTYAARTGW 376
Qy 335 GGATCCAGACTCCGACAAATGTTGGCAATTGGTAATAATATTAAGATTGAATTA 394

Db 377 SNGAGAYGAYYTNABACNGTNTTYGCMCACTTGGNCGNTNYNGARTNAAYATHC 436
Qy 395 TTTTAA---TGAGCGGGCTCGAAGGATTTGGTTGTCTAATTTCGAAAATAGCGCG 451
Db 437 CMAAGARARAGGNAARAAAGAAAYWSNGARTGVCNABARARAGCCNABARAG 496
Qy 452 ATCCGACAGGCGGAGGAAATTCACAGGTACCGGTGTAGAGGCGCTTAATTCAGAG 511
Db 497 ARCCNABARAGCNTTNAARAGNATGAAYATGAAGARATTHABRGNMCACTGTCNG 556
Qy 512 TTAATATCGACAGACGCGGTGATGATTAATTA 547
Db 557 TNGAYTGGCGNCTGNCNABARAGAYAAATYAARGAYA 592

RESULT 13

US-08-676-974-2
Sequence 2, Application US/08676974
Patent No. 5770422
GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,974
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Osman Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-676-974-2

Query Match 3.4%; Score 45; DB 1; Length 2277;

Best Local Similarity 32.4%; Pred. No. 0.0096;
Matches 109; Conservative 46; Mismatches 178; Indels 3; Gaps 1;

Qy 215 CCACACAGACAGATATGTCGCGCCCGACGAGCGCCGACGACCAACCTTCTGA 274
Db 257 CNAAGARARAGGNAARAAAGAAAYWSNGARTGVCNABARARAGCCNABARAG 316
Qy 275 ACACAGAAAACAAGTCCGACGCGCAAGCGGTGATGTCTCAATCCCTTCGGTTC 334
Db 317 ARCCNABRGTCNGAFAAARABGACNMGNTYNAATHMGNAAYTNWSTTYAARTGW 376
Qy 335 GGATCCAGACTCCGACAAATGTTGGCAATTGGTAATAATATTAAGATTGAATTA 394
Db 377 SNGAGAYGAYYTNABARAGNATGAAYATGAAGARATTHABRGNMCACTGTCNG 436
Qy 395 TTTTAA---TGAGCGGGCTCGAAGGATTTGGTTGTCTAATTTCGAAAATAGTGC 451

Qy	529	CGCGTG	534
Db	682	CGACTG	687

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
65.784 Million cell updates/sec

Title: US-09-809-545a-2

Perfect score: 1086
Sequence: 1 MTRKKAVPNTGKMLNPVY.....VLSSLOASTYOGGYNFAPY 203

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Gapop 10.0 , Gapext 0.5

Searched: 762491 seqs, 20448190 residues

Total number of hits satisfying chosen parameters: 762491

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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11: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubppaa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	551	50.7	330	9	US-09-794-591-2
3	519	47.8	450	12	US-10-094-749-1926
4	288	26.5	366	12	US-10-359-385-2
5	116	10.7	3063	12	US-10-301-822-26
6	116	10.7	3063	15	US-10-177-293-61
7	116	10.7	3063	15	US-10-177-293-61
8	96	8.8	388	12	US-10-012-952a-172
9	96	8.8	760	8	US-08-754-311b-2
10	94.5	8.7	950	12	US-10-108-260a-4492
11	93	8.6	692	15	US-10-156-761-14649
12	92.5	8.5	919	15	US-10-128-714-8387
13	92	8.5	351	12	US-10-029-386-32088
14	90.5	8.3	481	15	US-10-156-761-12012
15	90	8.3	443	12	US-10-369-493-10023

16	89.5	8.2	342	15	US-10-156-761-11221	Sequence 11221, A
17	89	8.2	470	12	US-10-104-047-2022	Sequence 2022, Ap
18	88.5	8.1	363	15	US-10-156-761-10205	Sequence 10205, A
19	88	8.1	380	15	US-10-156-761-11952	Sequence 11952, A
20	88	8.1	216	12	US-10-224-999a-3475	Sequence 3475, Ap
21	87.5	8.1	620	15	US-10-156-761-7979	Sequence 7979, Ap
22	87	8.0	465	15	US-10-205-823-136	Sequence 136, App
23	87	8.0	2135	12	US-10-329-079-43	Sequence 43, App
24	86.5	8.0	262	10	US-09-263-689-14	Sequence 14, App
25	86.5	8.0	262	15	US-10-235-674-14	Sequence 14, App
26	86.5	8.0	742	15	US-10-156-761-12153	Sequence 12153, A
27	86.5	8.0	4292	12	US-10-080-334-273	Sequence 273, App
28	86.5	8.0	4299	12	US-10-080-334-90	Sequence 90, App
29	86.5	8.0	4302	12	US-10-080-334-271	Sequence 271, App
30	86.5	8.0	4302	12	US-10-080-334-272	Sequence 272, App
31	86	7.9	245	9	US-09-796-858-20	Sequence 20, App
32	86	7.9	275	12	US-10-313-853-3	Sequence 3, App
33	86	7.9	279	11	US-09-813-408-21	Sequence 21, App
34	86	7.9	337	15	US-10-156-761-12003	Sequence 12003, A
35	86	7.9	518	12	US-10-369-493-3240	Sequence 3240, Ap
36	86	7.9	550	15	US-10-156-761-11905	Sequence 11905, A
37	86	7.9	853	12	US-10-369-493-15517	Sequence 15517, A
38	86	7.9	856	12	US-10-369-493-15889	Sequence 15889, A
39	86	7.9	856	12	US-10-369-493-16260	Sequence 16260, A
40	85	7.8	275	8	US-08-322-678-7	Sequence 7, App
41	85	7.8	275	9	US-09-060-854B-3	Sequence 3, App
42	85	7.8	275	10	US-09-976-414-7	Sequence 7, App
43	85	7.8	275	12	US-10-324-152-1	Sequence 1, App
44	85	7.8	275	12	US-09-824-607-1	Sequence 1, App
45	85	7.8	275	12	US-10-242-549-4	Sequence 4, App

ALIGNMENTS

RESULT 1
US-09-809-545a-2
; Sequence 2, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Scanlon, Lawrence W.
; APPLICANT: White, R. Tyler
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS.017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-809-545a-2

Query Match	100.0%;	Score 1086;	DB 10;	Length 203;
Best local Similarity	100.0%;	Pred. No. 1.4e-98;		
Matches 203;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MTRKKAVPNTGKMLNPVGAIVSPDFYAGTVLLCQANQEGSSMYGSPSLVYTSAMFG	60	
DB	1	MTRKKAVPNTGKMLNPVGAIVSPDFYAGTVLLCQANQEGSSMYGSPSLVYTSAMFG	60	
QY	61	FEYPATATAAARGAHLRGRTVNTTPAALPPPIPAVGGVVOEPYKGLIOGGA	120	
DB	61	FEYPATATAAARGAHLRGRTVNTTPAALPPPIPAVGGVVOEPYKGLIOGGA	120	
QY	121	AYRYAOPTPATAAASDSYGRYAADPYHTTLAPYTVGVGAMNAPALTDKTSHAD	180	
DB	121	AYRYAOPTPATAAASDSYGRYAADPYHTTLAPYTVGVGAMNAPALTDKTSHAD	180	
QY	181	VELVLSLOASTYOGGYNFAPY 203		
DB	181	VELVLSLOASTYOGGYNFAPY 203		
QY	181	VELVLSLOASTYOGGYNFAPY 203		
DB	181	VELVLSLOASTYOGGYNFAPY 203		

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RESULT 2
US-09-794-591-2
; Sequence 2, Application US/09794591
; Patent No. US20010018198A1
; GENERAL INFORMATION:
; APPLICANT: Pulec, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/794,591
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/145,391
; PRIOR FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-794-591-2

Query Match      50.7%; Score 551; DB 9; Length 330;
Best Local Similarity 97.1%; Pred. No. 7,7e-46;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1  MTNKKAVNPTNGMKLNPPVGVAYSPDPFYAGTVLLCOANOGSSMYGSPSSLYVTSAMPG 60
        |||||
DB      196  MTNKKTNPTNGMKLNPPVGVAYSPDPFYAGTVLLCOANOGSSMYGSPSSLYVTSAMPG 255
        |||||

QY      61  PPVPAATAAAAYRGAGHLRGRGRTYNTFRFAAAPPPPIPAYGVVY 105
        |||||
DB      256  PPVPAATAAAAYRGAGHLRGRGRTYNTFRFAAAPPPPIPAYGVVY 300
        |||||

RESULT 3
US-10-094-749-1926
; Sequence 1926, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOUYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1926
; LENGTH: 450
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
US-10-094-749-1926

Query Match      47.8%; Score 519; DB 12; Length 450;
Best Local Similarity 52.3%; Pred. No. 1.6e-42;
Matches 115; Conservative 14; Mismatches 45; Indels 46; Gaps 8;

QY      1  MTNKKAVNPTNGMKLNPPVGVAYSPDPFYAGTVLLCOAN--OEGSSMYGSPSS-----L 52
        |||||
DB      260  MTNKKAVNPTNGMKLNPPVGVAYSPDPFYAGTVLLCOANAVPLSGRGGINTYIPL 319
        |||||

QY      53  VYTSAMPGRFPY-AAATAAAYRGAGHLRGRGRTYNTFRFAAAPPPPIPAYGVVYQGFYV 111
        :|||
DB      320  ISLPLVPGFPYPTAATTAAFRGAGHLRGRGRTYVAVR-AVPEPTALPAYGVVYQGFYV 378
        :|||

QY      112  NKLLGGYAAVRYAOPTPAT-----AAAYSDSYGRVYAADPYHHTLAPAPTYVGAM 163
        |||||
DB      379  AD-LYGGYAAVRYAOPATATTAATAAATAAAYDGYGRYTTADPY-HALAPASVGVAV 436
        |||||

QY      164  NAFAPLTDKTRSHADVGLVLSLQASLYGGYRFPAY 203
        |||||
DB      437  -----ASLYRGYSRFPAY 450
        |||||

RESULT 4
US-10-359-385-2
; Sequence 2, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bardenan, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-10-359-385-2

Query Match      26.5%; Score 288; DB 12; Length 366;
Best Local Similarity 48.9%; Pred. No. 5.4e-20;
Matches 68; Conservative 11; Mismatches 54; Indels 6; Gaps 4;

QY      1  MTNKKAVNPTNGMKLNPPVGVAYSPDPFYAGTVLLCOAN--OEGSSMYGSPSSL--VYTS 56
        |||||
DB      190  MTNKKAVNPTNGMKLNPPVGVAYSPDPFYAGTVLLCOANAVPLSGRGGINTYIPL 249
        |||||

QY      57  AMRGPFPY-AAATAAAYRGAGHLRGRGRTYNTFRFAAAPPPPIPAYGVVYQGFYVGNKLL 115
        :|||
DB      250  IIRGFPYPTAATTAAFRGAGHLRGRGRTYVAVR-AVPEPTALPAYGVVYQGFYV 308
        :|||

QY      116  QGGYAAVRYAOPTPATTA 134
        :|||
DB      309  QPQPLLPPLQPLTLTYVMA 327
        :|||

RESULT 5
US-10-301-822-26
; Sequence 26, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
```


APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
THERAPY OF COLON CANCER
FILE REFERENCE: MEMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ. ID NOS: 228
SOFTWARE: FastSeq for Windows Version 4.0
SEQ. ID NO 26
LENGTH: 3063
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-301-822-26

Query Match 10.7%; Score 116; DB 12; Length 3063;
Best Local Similarity 25.1%; Pred. No. 0.058;
Matches 45; Conservative 16; Mismatches 54; Indels 64; Gaps 8;
QY 50 SSLVYTSAMPGFPPYATATAAAYR---GAHLRGGRTV-----YNTFRRAA 92
DB 2078 NNVILOPLQDTPY-KITVIAVYEDDGGHLTGNGRTVGLPPQNIHISDEWTRFRVSM 2136
QY 93 PPPPIYAGGVVYQEPYVGNKLLQ---GGYAAARYAQPFPATAAAYSDSYGRVYADPYH 149
DB 2137 DPEPSVVLGKYIKVYKPGVSNPEMEAFVGEWTSYTL----- 2171
QY 150 HTLAAPATYGVGAMNAFA-----PLTDKTRSHADVDGLVLSLQASITYGGYNRF 200
DB 2172 HNINPSTTYDV--NVYAQYDSGLSVPLTDQGT-----LYLNVTLKTYQIGMDTF 2220

RESULT 6
US-10-177-293-61
Sequence 61, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatc, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannavarpu, Manjula
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Pusztai, Lajos
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ. ID NOS: 506
SOFTWARE: FastSeq for Windows Version 4.0
SEQ. ID NO 61
LENGTH: 3063
TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-293-61

Query Match 10.7%; Score 116; DB 15; Length 3063;
Best Local Similarity 25.1%; Pred. No. 0.058;
Matches 45; Conservative 16; Mismatches 54; Indels 64; Gaps 8;
QY 50 SSLVYTSAMPGFPPYATATAAAYR---GAHLRGGRTV-----YNTFRRAA 92
DB 2078 NNVILOPLQDTPY-KITVIAVYEDDGGHLTGNGRTVGLPPQNIHISDEWTRFRVSM 2136
QY 93 PPPPIYAGGVVYQEPYVGNKLLQ---GGYAAARYAQPFPATAAAYSDSYGRVYADPYH 149
DB 2137 DPEPSVVLGKYIKVYKPGVSNPEMEAFVGEWTSYTL----- 2171
QY 150 HTLAAPATYGVGAMNAFA-----PLTDKTRSHADVDGLVLSLQASITYGGYNRF 200
DB 2172 HNINPSTTYDV--NVYAQYDSGLSVPLTDQGT-----LYLNVTLKTYQIGMDTF 2220

RESULT 7
US-10-177-293-63
Sequence 63, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatc, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannavarpu, Manjula
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Pusztai, Lajos
APPLICANT: Sahin, Aysegul
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25

PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 63
LENGTH: 3063
TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-293-63

Query Match 10.7%; Score 116; DB 15; Length 3063;
Best Local Similarity 25.1%; Pred. No. 0.058;
Matches 45; Conservative 16; Mismatches 54; Indels 64; Gaps 8;

QY 50 SSLVTSAMPGEFPPYPAATAAAAYR---GAHLRGKRTV-----YTFPAAA 92
DB 2078 NNVLQPLQPDTPY-KITVIAVYEDGDGGLTGNGRTVGLLPQNIHISDEMYTRFRVSW 2136
QY 93 PPPPIPAYGVVYQEPYGNKLLQ---GVYAAVRYAPTRATATAAAYSDYGRVYAADPYH 149
DB 2137 DPSSPVLGKIKYKPKVGSNEPMEAFVGEWTSYTL----- 2171
QY 150 HTLAPARTYGVGAMNAPF-----PLTDKTRSHADVDGLVLSIQAGSYQGYNRF 200
DB 2172 HNLNPSITTYDV---NVYAAQYDSGLSVLTLQGT-----LYNVTDKTKYQIGWTF 2220

RESULT 8
US-10-012-952A-172
Sequence 172; Application US/10012952A
Publication No. US20030175707A1
GENERAL INFORMATION:
APPLICANT: Sun, Yongming
APPLICANT: Recipon, Herve
TITLE OF INVENTION: Composition and Methods Relating to Prostate Specific Genes and F
FILE REFERENCE: DEX-0263
CURRENT APPLICATION NUMBER: US/10/012,952A
PRIOR FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/246,039
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.1
SEQ ID NO 172
LENGTH: 388
TYPE: PRT
ORGANISM: Homo sapiens
US-10-012-952A-172

Query Match 8.8%; Score 96; DB 12; Length 388;
Best Local Similarity 24.9%; Pred. No. 0.4;
Matches 59; Conservative 16; Mismatches 86; Indels 76; Gaps 11;

QY 21 GAVVSPDYAGTVLLCANDEGSSMYSGPSL-----VYTSAMPGEFPPYPAATAAAAYRG 74
DB 67 GGNSTVAAAAAANAQ-CRNLMAHFAFLAAGASAYSSA-PGEAFPSAAAAA 124
QY 75 AHLRGKRTVYNTFRFAAARPPPIPAYGVVYQ-----EPYVGNKLLQGYAAYRY- 124
DB 125 A-----AAAAAASSSGRPGAGAGAAKQCSPCSAAAOSSGPAALPYGYFGSGYYP 180
QY 125 -----AQTPTATAA-----YSDS-----YGRVYAADPY 148
DB 181 CARMGPHNAIKSCAQFASAAAAAFADKYMDTAGPAAEBSFSAKEFAFYHOGYAAAGPY 240
QY 149 HHTLAPARTY-----GVGAMNAPARTLDAKTRSHADVDGLVLSIQAGSYQGYN 198
DB 241 HHN-OPMFGYLDMPVYPLGSGPG-----ESRHEPLGPMESYOPALPMGN 286

RESULT 9

US-08-754-311B-2
Sequence 2; Application US/08754311B
Publication No. US20020004221A1
GENERAL INFORMATION:
APPLICANT: Bonini, Nancy M.
APPLICANT: Leiserson, William M.
TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fleht, Hobach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/754,311B
FILING DATE: 21-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/195,152
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Treacartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-59551/RFT/RMS
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 760 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-754-311B-2

Query Match 8.8%; Score 96; DB 8; Length 760;
Best Local Similarity 23.7%; Pred. No. 0.92; Indels 50; Gaps 6;
Matches 42; Conservative 24; Mismatches 61

QY 42 GSSNY-----SGPSSLVYTSAMPGEFPPYPAATAAAAYRGALRGKRTVYNTFRFAA 92
DB 223 GSNLYGSSASNPDLGGAIVAVNSAV-----AAAAAAYDGH-----DYTYNSMQOYT 272
QY 93 PPPPIPAYGVVYQEPYGNKLLQGYAAYRYAQTPTATAA----- 134
DB 273 PPPFYSYGGPYAATAARQAKPEPGAAAAAAYLTPSYAAGNNNSQLYSSPYAGYNF 332
QY 135 -----YDSYGRVYAADPYHHTLAPAR-----TYGVG-AMNAPARTLDAKTRSHA 178
DB 333 GOODYGGYVNEQYNTSPANYSPYAVVSSSSASHGKHVAAASSLSLSPFDTHS 389

RESULT 10
US-10-108-260A-4492
Sequence 4492; Application US/10108260A
Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: Helix Research Institute
TITLE OF INVENTION: No. US20040005560a1 full length cDNA
FILE REFERENCE: H1-40106
CURRENT APPLICATION NUMBER: US/10/108,260A
FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458

SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4492
 LENGTH: 950
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-108-2604-4492

Query Match 8.7%; Score 94.5; DB 12; Length 950;
 Best Local Similarity 25.0%; Pred. No. 1.7;
 Matches 35; Conservative 15; Mismatches 51; Indels 39; Gaps 6;

QY 39 NQCGSSMSYSGPSSLVYTSAMPGEPPYPAATAAAAYGCAHLRGRTVYNTFRAAAPPPPP 98
 DB 836 DQSEPPFPVPPGGYMYTVLPDGSFVP-----GGMALY-----APPPPLP 874
 QY 99 -----AYGVVYQEPYVYKLLQGGAAYRYAOPFPATAAASDSYGRVYADPYHHTL 152
 DB 875 NNSRPLTPGTIVYVGGPPAGAPMYG-----PPPNPSIPFPIMGVLIHCNVPEHHNL 925
 QY 153 APAPTYGVGAMNAFAP-LTD 171
 DB 926 VSGKTY--NSLSTLTPWMTD 943

RESULT 11
 US-10-156-761-14649
 Sequence 14649, Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHITOKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT APPLICATION NUMBER: US/10/156,761
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 14649
 LENGTH: 692
 TYPE: PRT
 ORGANISM: Streptomyces avermitilis
 US-10-156-761-14649

Query Match 8.6%; Score 93; DB 15; Length 692;
 Best Local Similarity 31.1%; Pred. No. 1.6;
 Matches 42; Conservative 8; Mismatches 47; Indels 38; Gaps 8;

QY 42 GSSMSYSGPSSLVYTSAMPGEPPYPAATAAAAYG-----AHLRGRTVYNTFRAAAP-- 93
 DB 329 GIGANGVPGGTGSGAGSAPSPPGATAGTAGTGTSSEPPGVGPAAGSGGDPNAPFYA 388
 QY 94 -PPPIAYGVVYQEPYVYKLLQGGAAYRYAOPFPATAAAY-----SDSYGRVYA 144
 DB 389 HDPATPSYG-----QEP-----GAPRGPPTASPYGRSPTASPYGSPRA 428
 QY 145 ADPYHHTLAPAPTYG 159
 DB 429 ATPYADPTASP-YG 442

RESULT 12
 US-10-128-714-8387
 Sequence 8387, Application US/10128714
 Publication No. US20030119013A1
 GENERAL INFORMATION:

APPLICANT: Jiang, Bo
 APPLICANT: Hu, Wengqi
 APPLICANT: Tishkoff, Daniel
 APPLICANT: Zamudio, Carlos
 APPLICANT: Eroethkin, Alexey M
 APPLICANT: Lemieux, Sebastien M
 TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
 FILE REFERENCE: 10182-018-999
 CURRENT APPLICATION NUMBER: US/10/128,714
 CURRENT FILING DATE: 2002-04-23
 PRIOR APPLICATION NUMBER: US 60/285,697
 PRIOR FILING DATE: 2001-04-23
 PRIOR APPLICATION NUMBER: US 60/287,066
 PRIOR FILING DATE: 2001-04-27
 PRIOR APPLICATION NUMBER: US 60/295,890
 PRIOR FILING DATE: 2001-06-05
 PRIOR APPLICATION NUMBER: US 60/303,899
 PRIOR FILING DATE: 2001-07-09
 PRIOR APPLICATION NUMBER: US 60/316,362
 PRIOR FILING DATE: 2001-08-31
 NUMBER OF SEQ ID NOS: 8603
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 8387
 LENGTH: 919
 TYPE: PRT
 ORGANISM: Aspergillus fumigatus
 US-10-128-714-8387

Query Match 8.5%; Score 92.5; DB 15; Length 919;
 Best Local Similarity 28.6%; Pred. No. 2.6;
 Matches 36; Conservative 10; Mismatches 61; Indels 19; Gaps 5;

QY 57 AMPGPPYPAATAAAAYGCAHLRGRTVYNTFRAAAPPPPIAYGVVYQEPYVYKLLQ 116
 DB 47 AYAGEAFBIGSANAALGGOLPAGS--YGAY-----PPQQAAG--YQGVYGADEPQ 96
 QY 117 GGAAYRYAOPFPATAAASDSYGRVYADPYHHTLAPAPTYGVGAMNAFAPL----- 169
 DB 97 MNAABGYTAPVTPTGLAQNTQPGAMGVDP--HLMPQPPQAAVAPQAPRVPLNQLYP 154
 QY 170 TDAKTR 175
 DB 155 TDLTQ 160

RESULT 13
 US-10-029-386-32088
 Sequence 32088, Application US/10029386
 Publication No. US20030194704A1
 GENERAL INFORMATION:
 APPLICANT: Penn, Sharon G.
 APPLICANT: Rank, David K.
 APPLICANT: Hanzel, David K.
 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 FILE REFERENCE: AEWICA-X-2
 CURRENT APPLICATION NUMBER: US/10/029,386
 CURRENT FILING DATE: 2001-12-20
 NUMBER OF SEQ ID NOS: 34288
 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 32088
 LENGTH: 351
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO L39891.1
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.4
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 11
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.4
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.6
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.9

OTHER INFORMATION: SWISSPROT HIT: P98161, EVALUATE 5.00e-39
US-10-029-386-32088

Query Match
Best Local Similarity 24.5%; Score 92; DB 12; Length 351;
Matches 58; Conservative 24; Mismatches 83; Indels 72; Gaps 11;

QY 18 PVVGAAY---SPFVAGTVLLCOANQEGSSMYSGPSSLVYTSAMPFPYPA-----66
DB 125 PLIGEEVYACLPDNGSGTV-----AAVSSAAHEGLLOEACAFCFST 168
QY 67 ---TAAAYRGALHGRGRVYNTFR---AAAPPPPIAYGQVYQEPVY-----110
DB 169 GQGLAALSEQGWLCCGAAGPSSASFACTLSCGPPPPAPTCRGPILLQHVFPASPQATL 228
QY 111 ---GNKLLQGGYAAVRYAOTPTATAA--YSDSYGRYAADP-----YHHTLAP 154
DB 229 VGPBGPILASQOLAFAHIAFLPYATRTWDPDGSAAEVDAAGPASHRYVLPGRYHTVAVL 288
QY 155 APYVGVANNAFAPLTDKTRSHADVDVGLV-----SSLOASTY-QGGVNRFPAPY 203
DB 289 A----LGAGSALLG-IDVQVEAPALAEIVCPSSVQSDSLDSIQNRGSSGLEAAY 340

RESULT 14
US-10-156-761-12012

Sequence 12012, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12012
LENGTH: 481
TYPE: PRT
ORGANISM: Streptomyces avermectilis
US-10-156-761-12012

Query Match
Best Local Similarity 28.0%; Score 90.5; DB 15; Length 481;
Matches 47; Conservative 11; Mismatches 75; Indels 35; Gaps 7;

QY 26 PDPVAGTVLLCOANQEGSSMYSGPSS---LVYTS-AMPFPYPAATAAAYRGALHGR 80
DB 298 PDESSGANVLLIRFGADAGGASGESGRKTCISQSSBGVPTAEPGDAMGASVAAADDDG 357
QY 81 GRVYNTFRFAAAPPPPIAYG-----GVVYQEPVYQGNKLLQGGYAAVRYAOTPTAT 131
DB 358 G-----APELVVGAPGEGVSLKSGSVTVLDGTGEGPLSGGVT---YTONTPCI 404
QY 132 ---AAAYSDSYGRVYAADPYHHTLAPAPYVGVANNA-----FAPLTD 171
DB 405 PGTAEIADRFAGATLTAGPYHGRPDLAIGAPGENAAKGWVYVPTTD 452

RESULT 15
US-10-369-493-10023
Sequence 10023, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 10023
LENGTH: 443
TYPE: PRT
ORGANISM: magneticite-containing magnetic coccus
US-10-369-493-10023

Query Match
Best Local Similarity 26.2%; Score 90; DB 12; Length 443;
Matches 49; Conservative 14; Mismatches 56; Indels 68; Gaps 11;

QY 17 NPVGAAYSPDPFYAGT-----VLLCOANQEGSSMYSGPSSLVYTSAMPFPYPAATA 69
DB 48 SPVAGVI--TEIYAGVADADVEGAVLCVDAQGSAAVAVPAK---PAAEPA-PAPAVATA 101
QY 70 AAYRGALHGRGRVYNTFRFAAAPPPPIA---YGVYQEPVY-----109
DB 102 ATPAPA-----VATPAPTVPVAPPSGGAALSPAVRKLAEHGLDATTQIPAT 147
QY 110 -YGNKLLQGGYAAV-----RYAOTPTATAAAYSDSYGRVYAADPYHHTLAPAPYVGV 161
DB 148 GSGGRLTKGDVLAIVLEQPKAPAPTAAPTAPTAAPT-----APTP---TPADAPM-----194
QY 162 ANNAFAP 168
DB 195 ATPALAP 201

Search completed: January 15, 2004, 09:02:14
Job time : 634 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 15, 2004, 06:09:58 ; Search time 45 Seconds
(without alignments)
190.869 Million cell updates/sec

Title: US-09-809-545A-2

Perfect score: 1086
Sequence: 1 MTNRKAVNPYNGMKLNPVY.....VLSSQASIVQSGYNFAPY 203

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patente_AA:*

- 1: /cgn2_6/prodata/2/1aa/5A COMB .pep:*
- 2: /cgn2_6/prodata/2/1aa/5B COMB .pep:*
- 3: /cgn2_6/prodata/2/1aa/6A COMB .pep:*
- 4: /cgn2_6/prodata/2/1aa/6B COMB .pep:*
- 5: /cgn2_6/prodata/2/1aa/PCTUS COMB .pep:*
- 6: /cgn2_6/prodata/2/1aa/backfile1 .pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	50.7	330	3 US-09-145-391-2	Sequence 2, Appl1
2	288	26.5	366	3 US-09-176-657-2	Sequence 2, Appl1
3	288	26.5	366	4 US-09-421-299-2	Sequence 2, Appl1
4	96	8.8	760	1 US-08-195-152-2	Sequence 2, Appl1
5	94	8.7	349	4 US-09-143-011B-1	Sequence 1, Appl1
6	93	8.6	444	3 US-09-252-292C-27	Sequence 27, Appl1
7	92.5	8.5	362	1 US-08-437-027-21	Sequence 21, Appl1
8	92.5	8.5	365	1 US-08-437-027-20	Sequence 20, Appl1
9	92.5	8.5	656	2 US-08-343-443B-2	Sequence 2, Appl1
10	92.5	8.5	656	2 US-09-214-564A-4	Sequence 4, Appl1
11	91	8.4	346	4 US-09-343-011B-2	Sequence 2, Appl1
12	88.5	8.1	902	4 US-09-252-991A-119897	Sequence 19897, A
13	87.5	8.1	980	4 US-09-442-100-8	Sequence 8, Appl1
14	87.5	8.1	980	4 US-08-939-106-8	Sequence 8, Appl1
15	87	8.0	379	1 US-08-552-142A-11	Sequence 11, Appl1
16	86.5	8.0	262	4 US-08-946-914-14	Sequence 14, Appl1
17	86.5	8.0	262	4 US-09-656-450-14	Sequence 14, Appl1
18	86.5	8.0	4302	3 US-08-658-136-5	Sequence 5, Appl1
19	86.5	8.0	4302	4 US-09-052-469-8	Sequence 8, Appl1
20	86.5	8.0	4302	4 US-08-422-582-8	Sequence 8, Appl1
21	86.5	8.0	4339	4 US-09-052-469-6	Sequence 6, Appl1
22	86.5	8.0	4339	4 US-08-422-582-6	Sequence 6, Appl1
23	86	7.9	207	4 US-09-336-536-50	Sequence 50, Appl1
24	86	7.9	245	4 US-09-336-536-48	Sequence 48, Appl1
25	85	7.8	273	4 US-09-088-912-1	Sequence 1, Appl1
26	85	7.8	275	1 US-08-431-387-3	Sequence 3, Appl1
27	85	7.8	275	1 US-08-322-677A-7	Sequence 7, Appl1

28	85	7.8	275	1 US-08-322-676-7	Sequence 7, Appl1
29	85	7.8	275	1 US-08-460-343B-74	Sequence 74, Appl1
30	85	7.8	275	1 US-08-398-028B-74	Sequence 74, Appl1
31	85	7.8	275	2 US-08-504-265B-90	Sequence 90, Appl1
32	85	7.8	275	2 US-08-140-083A-9	Sequence 9, Appl1
33	85	7.8	275	2 US-08-865-203-8	Sequence 8, Appl1
34	85	7.8	275	2 US-09-135-658-3	Sequence 3, Appl1
35	85	7.8	275	2 US-07-849-420-8	Sequence 8, Appl1
36	85	7.8	275	3 US-08-898-218-7	Sequence 7, Appl1
37	85	7.8	275	3 US-08-848-793-7	Sequence 7, Appl1
38	85	7.8	275	3 US-09-253-854-8	Sequence 8, Appl1
39	85	7.8	275	3 US-08-955-424-8	Sequence 8, Appl1
40	85	7.8	275	4 US-09-178-155-3	Sequence 3, Appl1
41	85	7.8	275	4 US-09-445-270-2	Sequence 2, Appl1
42	85	7.8	275	4 US-09-467-536A-2	Sequence 2, Appl1
43	85	7.8	275	4 US-09-234-957-2	Sequence 2, Appl1
44	85	7.8	275	4 US-08-394-011-1	Sequence 1, Appl1
45	85	7.8	275	4 US-08-397-329-1	Sequence 1, Appl1

ALIGNMENTS

```
RESULT 1
US-09-145-391-2
; Sequence 2, Application US/09145391
; Patent No. 6194171
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; TITLE OF INVENTION: Products Related Thereto and Methods of Using Same
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/145,391
; CURRENT FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-145-391-2

Query Match      50.7% Score 551; DB 3; Length 330;
Best Local Similarity 97.1%; Pred. No. 3 4e-48;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 MTNRKAVNPYNGMKLNPVGAIVSBDPFACTVLLCQANQEGSSMYSGPSSLVYTSAMPG 60
      |||||
Db      196 MTNRKAVNPYNGMKLNPVGAIVSBDPFACTVLLCQANQEGSSMYSGPSSLVYTSAMPG 255
      |||||

QY      61 FYPPATATAAAYRGALHRRGRVTYNTFPAAPAPPPPIPAVGIVY 105
      |||||
Db      256 FYPPATATAAAYRGALHRRGRVTYNTFPAAPAPPPPIPAVGIVY 300
      |||||

RESULT 2
US-09-176-657-2
; Sequence 2, Application US/09176657
; Patent No. 6020164
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guebler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Marian R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/176,657
; CURRENT FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
```

```
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-09-176-657-2
```

```
Query Match          26.5%; Score 288; DB 3; Length 366;
Best Local Similarity 48.9%; Pred. No. 2.4e-21;
Matches 68; Conservative 11; Mismatches 54; Indels 6; Gaps 4;
```

```
QY 1 MTNKKAVNPYNGKLNPNVGVAVSPDYAGTVLLCOAN--QEGSSMYSGPSSL--VYTS 56
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 190 MTNKKAVNPYNGKLNPNVGVAVSPDYAGTVLLCOAN--QEGSSMYSGPSSL--VYTS 249
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 57 AMPGFPYP-AATAAAYRGALRGGRVTYNTFPRAAAPPPIPAYGVVYQEPYGNKLL 115
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 250 IIFGFPYPTAATYTAARGAHLRGGRVTYGVAVR-AVPTAIPAYPGVDMPDTMHSILL 308
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 QGGYAAYRYAQPPTATAA 134
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 309 QPQPLQLQPLQPLTVTMA 327
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 3

```
US-09-421-299-2
; Sequence 2, Application US/09421299
; Patent No. 6524579
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guebler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/421,299
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: 09/176,657
; EARLIER FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-09-421-299-2
```

```
Query Match          26.5%; Score 288; DB 4; Length 366;
Best Local Similarity 48.9%; Pred. No. 2.4e-21;
Matches 68; Conservative 11; Mismatches 54; Indels 6; Gaps 4;
```

```
QY 1 MTNKKAVNPYNGKLNPNVGVAVSPDYAGTVLLCOAN--QEGSSMYSGPSSL--VYTS 56
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 190 MTNKKAVNPYNGKLNPNVGVAVSPDYAGTVLLCOAN--QEGSSMYSGPSSL--VYTS 249
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 57 AMPGFPYP-AATAAAYRGALRGGRVTYNTFPRAAAPPPIPAYGVVYQEPYGNKLL 115
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 250 IIFGFPYPTAATYTAARGAHLRGGRVTYGVAVR-AVPTAIPAYPGVDMPDTMHSILL 308
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 116 QGGYAAYRYAQPPTATAA 134
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 309 QPQPLQLQPLQPLTVTMA 327
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 4
US-08-195-152-2
; Sequence 2, Application US/08195152
; Patent No. 5679541
```

```
; GENERAL INFORMATION:
; APPLICANT: Bonini, Nancy M.
; APPLICANT: Leiserson, William M.
; APPLICANT: Benzer, Seymour
; TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Flehr, Hombach, Test, Albritton & Herbert
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,152
; FILING DATE: 14-FEB-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Treacartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-59551/RFT/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 760 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-195-152-2
```

```
Query Match          8.8%; Score 96; DB 1; Length 760;
Best Local Similarity 23.7%; Pred. No. 0.23;
Matches 42; Conservative 24; Mismatches 61; Indels 50; Gaps 6;
```

```
QY 42 GSSMY-----SSPSSLYVTSAMPFPYPAATAAAYRGALRGGRVTYNTFRAAA 92
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 223 GSNLYGSSASNSRLDGGAVAVNSAV-----AAAAAAYVDGG-----DYYYNSMQOYT 272
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 93 PPPPIPAYGVVYQEPYGNKLLQGGYAAYRYAQPPTATAA----- 134
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 273 PPPFSGYGTTPYAAATAARQAKMEPGAAAAAAYLTTPSYAASGNNNSQLYSSPYAGYNF 332
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 135 -----YSDSYGRVYAADPYHHTLAPAP---TYGVG-AMNAPAPLTDKTRSHA 178
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 333 GOODYGGYVNEQYNTYSPANYSPYAVSSSSASHGHVAAASNSLSSPDTDS 389
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 5

```
US-09-343-011B-1
; Sequence 1, Application US/09343011B
; Patent No. 6300473
; GENERAL INFORMATION:
; APPLICANT: Stephanie Richard
; TITLE OF INVENTION: SLM-1 AND SLM-2; NOVEL
; TITLE OF INVENTION: SAM68-LIKE MAMMALIAN PROTEINS
; FILE REFERENCE: A32561
; CURRENT APPLICATION NUMBER: US/09/343,011B
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: CA 2265271
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastsEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 349
```

TYPE: PRT
ORGANISM: Mus musculus
US-09-343-011B-1

Query Match
Best Local Similarity 30.7%; Score 94; DB 4; Length 349;
Matches 54; Conservative 11; Mismatches 51; Indels 60; Gaps 12;

73 RGALRGRTVNTF-----RAAAPPPPIPAAGVGVYQEPVGNKLLG----- 117
186 RGRGIRGRIRITPTASRRGAGVPPPPRGVLTFR---GTYTRGALPPPIARGV 242
118 -----GYAA--YRYAQPPTATA--AYSDSYGRVYAADPY--HTTLAPAT----- 157
243 PTPRAGTAAPVGR-APPAPDAVEYGDGGEYDDQTYEAVDNGVYPTQSVPE 301
158 ---YVGC---ANAPAPLTDATRSHADVGLVLSLOA---SITYGGINRPAFY 203
302 YVDYGHGVNEDAVDVAPEEMATTR-----SLKAPPPRSARAGY-REHPY 346

RESULT 6

US-09-252-292C-27
Sequence 27, Application US/09252292C
Patent No. 6245968
GENERAL INFORMATION:
APPLICANT: Boudec, Philippe
APPLICANT: Rodgers, Matthew
APPLICANT: Dumais, Florence
TITLE OF INVENTION: Mutated hydroxyphenylpyruvate dioxygenase, DNA
TITLE OF INVENTION: sequence and isolation of plants which contain such a
FILE REFERENCE: 5500*31
CURRENT APPLICATION NUMBER: US/09/252,292C
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 08/982,772
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 27
LENGTH: 444
TYPE: PRT
ORGANISM: Zea mays
US-09-252-292C-27

Query Match
Best Local Similarity 22.8%; Score 93; DB 3; Length 444;
Matches 51; Conservative 22; Mismatches 69; Indels 82; Gaps 10;

55 TSAMPGRPYPAATAAAYRGALRG--RGRVTYNTFRANAPPPIPAYGV-----V 104
112 TAAIPSPSAAARPAADHGLAVRAVALRVADADADAVAAAGARAFGPVLDGRGRL 171
105 YQBPVGNKLLGCGYAAVRYAQPPTATAAAYSDSYGRV-----YAADPYNH-----T 151
172 AVEVELVDVLR--YVSY-----PDGAAGEPFLPGFEVSAFGAADYGLSFDHIVGNVPE 225
152 LAPAPY-----GVGAM-----NAPALTD-----AKTRSH 177
226 LAPAAAFAGFTGFHEFAEFTTEDVGTAEGLSNMVMVANNSEVLLPLNPNVHGTGRSQ 285
178 -----ADYGLVLSLSLOASTIYOGGINRPAF 202
286 IQFLDHHGGPGVQHMALASDDVLRITREMQARSAMGCFEFMAP 329

RESULT 7

US-08-437-027-21
Sequence 21, Application US/08437027
Patent No. 5670317
GENERAL INFORMATION:
APPLICANT: Landanyi, Marc
APPLICANT: Gerald, William

TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
TITLE OF INVENTION: SMALL ROUND CELL TUMOR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,027
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 46416/JPW/CCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-437-027-21

Query Match
Best Local Similarity 27.9%; Score 92.5; DB 1; Length 362;
Matches 48; Conservative 10; Mismatches 73; Indels 41; Gaps 9;

29 YAGTVLLCA-NOEGSSMWGSSSLVYTSNMGFPYPAATAAAYRGALRGRTVNT 87
29 YAGTVLLCA-NOEGSSMWGSSSLVYTSNMGFPYPAATAAAYRGALRGRTVNT 87
29 YAGTVLLCA-NOEGSSMWGSSSLVYTSNMGFPYPAATAAAYRGALRGRTVNT 87
88 PRAAPPPPIPAAGVGVYQEPVGNKLLGCGYAAVRYAQPPTATAAAYSDSYGRVYADP 147
80 -----PTAPQ---AYSQPVQY-----GTGALDTTATVTTTQA-----SYAQS 116
148 YHHTLAPAPTYGVGAMNAPAPLTDKTRSHADVGLVLSLOASTIYOGGINR 199
117 AVGTQPAVYVAGQ-----QPAATAPTRPDGNKPTETSPQSS--TGSYNQ 160

RESULT 8

US-08-437-027-20
Sequence 20, Application US/08437027
Patent No. 5670317
GENERAL INFORMATION:
APPLICANT: Landanyi, Marc
APPLICANT: Gerald, William
TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
TITLE OF INVENTION: SMALL ROUND CELL TUMOR
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,027
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 46416/JPW/CCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-437-027-20

Query Match 8.5%; Score 92.5; DB 1; Length 365;
Best Local Similarity 27.9%; Pred. No. 0.19; Indels 41; Gaps 9;
Matches 48; Conservative 10; Mismatches 73; Indels 41; Gaps 9;

QY 29 YAGTVLLCOA-NOEGSSMTSGPSLVYTSAMPFPYPAATAAAYRGALHGRGRVYNT 87
DB 29 YAGTT---QAYGQSGYGTGPTDVSTYQAQTATYGTATVATSY-----GQPTGYTT 79
QY 88 FRAAAPPPPIPAVGAVVYOEPPVGNKLLGGVAAAYRYAOPTPATAAAYSDSYGRVYAADP 147
DB 80 -----PTAPQ-----AYSQPVQGY-----GTGAYDTTATVTTTQA-----SYAQS 116
QY 148 YHHTLAAPTYGAMNAPAPLTDKTRSHADVGLVLSLSQASIVGGYNR 199
DB 117 AYGTQPAYPAYGQ-----OPATAPTPRPDGKNKPTETSPQSS--TGGYNQ 160

RESULT 9
US-08-343-443B-2
Sequence 2, Application US/08343443B
Patent No. 5968734
GENERAL INFORMATION:
APPLICANT: Aurias, Alain
APPLICANT: Delattre, Olivier
APPLICANT: Desmaze, Chantal
APPLICANT: Melot, Thomas
APPLICANT: Peter, Martine
APPLICANT: Ploougastel, Beatrice
APPLICANT: Thomas, Gilles
TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
TITLE OF INVENTION: TRANSLOCATIONS
NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weiser & Associates
STREET: 230 South Fifteenth Street
CITY: Philadelphia
STATE: PA
COUNTRY: PA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/06123
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989,6121P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 656 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-343-443B-2

Query Match 8.5%; Score 92.5; DB 2; Length 656;
Best Local Similarity 27.9%; Pred. No. 0.43; Indels 41; Gaps 9;
Matches 48; Conservative 10; Mismatches 73; Indels 41; Gaps 9;

QY 29 YAGTVLLCOA-NOEGSSMTSGPSLVYTSAMPFPYPAATAAAYRGALHGRGRVYNT 87
DB 29 YAGTT---QAYGQSGYGTGPTDVSTYQAQTATYGTATVATSY-----GQPTGYTT 79
QY 88 FRAAAPPPPIPAVGAVVYOEPPVGNKLLGGVAAAYRYAOPTPATAAAYSDSYGRVYAADP 147
DB 80 -----PTAPQ-----AYSQPVQGY-----GTGAYDTTATVTTTQA-----SYAQS 116
QY 148 YHHTLAAPTYGAMNAPAPLTDKTRSHADVGLVLSLSQASIVGGYNR 199
DB 117 AYGTQPAYPAYGQ-----OPATAPTPRPDGKNKPTETSPQSS--TGGYNQ 160

RESULT 10
US-09-214-564A-4
Sequence 4, Application US/09214564A
Patent No. 6150515
GENERAL INFORMATION:
APPLICANT: Sharp, Phillip A.
APPLICANT: Zhou, Qiang
TITLE OF INVENTION: TAR-SF: Cofactor For Stimulation Of Transcriptional
TITLE OF INVENTION: Elongation By HIV-1 TAR
FILE REFERENCE: M0656/7042
CURRENT APPLICATION NUMBER: US/09/214,564A
PRIOR FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: US 60/021,218
PRIOR FILING DATE: 1996-07-03
PRIOR APPLICATION NUMBER: US 60/033,152
PRIOR FILING DATE: 1996-12-13
PRIOR APPLICATION NUMBER: PCT/US97/11713
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 656
TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-564A-4
Query Match 8.5%; Score 92.5; DB 3; Length 656;
Best Local Similarity 27.9%; Pred. No. 0.43; Indels 41; Gaps 9;
Matches 48; Conservative 10; Mismatches 73; Indels 41; Gaps 9;

Db 80 -----PTAPQ-----AYSQPVQGY-----GTGAYDPTTATVTTTQA-----SYAQS 116
 QY 148 YHHTLAPATPYGVGAMNAPFLDIAKTRSHADVDGLVLSLQASISYGGYNR 199
 Db 117 AYGTQPAYPAVAGQ-----QPAATAPTRPODGNKPTETSOPOS--TGTGYNQ 160

RESULT 11

US-09-343-011B-2
 ; Sequence 2, Application US/09343011B
 ; Patent No. 6306473
 ; GENERAL INFORMATION:
 ; APPLICANT: Stephane Richard
 ; TITLE OF INVENTION: SLIM-1 AND SLIM-2; NOVEL
 ; TITLE OF INVENTION: SAME68-LIKE MAMMALIAN PROTEINS
 ; FILE REFERENCE: A32561
 ; CURRENT APPLICATION NUMBER: US/09/343,011B
 ; CURRENT FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: CA 2265271
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 346
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-09-343-011B-2

Query Match
 Best Local Similarity 8.4%; Score 91; DB 4; Length 346;
 Matches 32; Conservative 8; Mismatches 46; Indels 10; Gaps 4;

QY 60 GFPPATATAAAYGAILRGRG-----RTVYNT-FRAAAPPPPIYGVYQEPYGN 112
 Db 221 GTPPRGVLT-RGPVSRGGLTPRAKGVPPGYRPPPPPTQTYGYDDG-YGT 277
 QY 113 KLQGGYAAAYRAOPTATAAAYSDSYGRVYADPY 148
 Db 278 AYDEQSYDSDNSTYTAQSNADYDYGHGLSEAY 313

RESULT 12

US-09-252-991A-19897
 ; Sequence 19897, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196,136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 19897
 ; LENGTH: 902
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-19897

Query Match
 Best Local Similarity 8.1%; Score 88.5; DB 4; Length 902;
 Matches 54; Conservative 19; Mismatches 75; Indels 81; Gaps 11;

QY 26 PDPTAGTVLLCOANQEGSSMYSGP-----SLVYTAMRGFPYPATATAAAYR 73
 Db 92 PGWYAGS-----RRNSGPRGPRRAGRATLPGSASRMARWAPAGSPRGPACR 146
 QY 74 GA-----HLGR-----GRTVNTFPAA--APPPIP-----AY 100

Db 147 GTATGWPRAADRHSAGCGPGRRIADEGKRAPDGRPPGPRGPARIHWRGFRGPASRAC 206
 QY 101 GGVVQEPYGNKLLQGGYAAAYRAVQPTPATAAAYSDSYGRVYADPYHNTLAP----- 154
 Db 207 ASVFOQLGTRQDQVVOG-----EAEVLEQRGRRLLEAGHADAPVETDYL 253
 QY 155 APTVGVGAMNAPFLDIAKTRSHADVDGLVLSLQASISYGGYNR 200
 Db 254 VPVVGMGGLDG-----DARADFHROHGLLVGLLVLDYD-----GAMHRY 293

RESULT 13

US-09-442-100-8
 ; Sequence 8, Application US/09442100
 ; Patent No. 6159193
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Tian
 ; APPLICANT: Tao, Wufan
 ; APPLICANT: Wang, Weiyl
 ; APPLICANT: Zhang, Sheng
 ; APPLICANT: Yu, Wan
 ; TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/442,100
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/411,111
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mastrock, S. Leslie
 ; REGISTRATION NUMBER: 18, 872
 ; REFERENCE/DOCKET NUMBER: 6523-003
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 980 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 US-09-442-100-8

Query Match
 Best Local Similarity 8.1%; Score 87.5; DB 4; Length 980;
 Matches 50; Conservative 21; Mismatches 81; Indels 45; Gaps 9;

QY 26 PDPTAGTVLLCOANQEGSSMYSGPSSLVYTAMP-----GFYPATATAAAYGAILRGRG 81
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 QY 82 RTVYNTFPRAAAPPPPIP-----AYGVVYQEPYV-----NKLQGGYAAAYRAVQ--- 126
 Db 163 PGWYAGS-----AVEPSAHPGTHYRGHLSQSGYGVQRSSSFQNKTPPDPAYSMAVAGGCP 220
 QY 127 ----PTPATAAAYSDSYGRVYADPYHNTLAPATYV---VGAMNAPFLDIAKTRSHAD 179

Db 221 PASLTFFPAHAGLYTASHHKPAATPPGAHPLHVLCTGRPTFGSSAQAVLAPSR----- 274
QY 180 DVGVLSSLOASIQOG 196
Db 275 -----NSLNADLYELG 285

RESULT 14

US-08-939-106-8
Sequence 8, Application US/08939106
Patent No. 6559285
GENERAL INFORMATION:
APPLICANT: Yale University
TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF LATS
GENES AND METHODS BASED THEREON
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,106
FILING DATE: 26-NOV-1997
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-007-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 980 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-08-939-106-8

Query Match 8.1%; Score 87.5; DB 4; Length 980;
Best Local Similarity 25.4%; Pred. No. 2.4; Indels 45; Gaps 9;
Matches 50; Conservative 21; Mismatches 81;
QY 26 PDFAVAGVLLCOAQEGSSSMYSGPSLSVYTSAMP-----GPPYPATAAAYRGALHRLRG 81
Db 108 PSFGSTGALPSYHQLGAGNVEGPAL--BEMPRQYUDFLPG--AGAGTHGAQHHP 162
QY 82 RTVNTTFPAAAPPPPIP-----AYGCVTVQEPVYG-----NKLLQGGYAAHYAQ-- 126
Db 163 PKGVST--AVEPSAHFPGTHYGRGHLSEQSGYGVQRSSSPONKTPPDAYSMSMAKAOQGP 220
QY 127 -----PTPATAAYSDSYGRVYAADPYHHTLAPAPYQ--VGAMNAFAPLTDAKTRSHAD 179
Db 221 PASLTFFPAHAGLYTASHHKPAATPPGAHPLHVLCTGRPTFGSSAQAVLAPSR----- 274
QY 180 DVGVLSSLOASIQOG 196
Db 275 -----NSLNADLYELG 285

RESULT 15
US-08-552-142A-11

Sequence 11, Application US/08552142A
Patent No. 5695995
GENERAL INFORMATION:
APPLICANT: Weintraub, Harold M.
APPLICANT: Lee, Jacqueline E.
APPLICANT: Tapscott, Stephen J.
APPLICANT: Hollenberg, Stanley M.
TITLE OF INVENTION: Neurogenic Differentiation (Neurod) Genes
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson KindnessPLLC
STREET: 1420 Fifth Avenue, Suite 2800
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/552,142A
FILING DATE: 02-NOV-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,238
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US95/05741
FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FPCR-1-8933
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-225-0709
TELEFAX: 206-682-8100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-552-142A-11

Query Match 8.0%; Score 87; DB 1; Length 379;
Best Local Similarity 20.8%; Pred. No. 0.74;
Matches 38; Conservative 23; Mismatches 73; Indels 48; Gaps 6;
QY 14 WKLNPPVGVANYSDFPFAVAGVLLC-----QANQEGSSMYSGP 49
Db 171 WALSEILRSKRDPDLVSIVYVTLCKLSQPTTNLVAGCLQNSNPLTEQGRDAXRPHGS 230
QY 50 SSLVYTSAMPGPFPAPAA-----TAAAYRGALHRLGRGR--TVYNT--FPAAAPPPPIPA 99
Db 231 GG--PFAAMPYIPPCGRGRGRTVPGAAAWAAAGRLRTHGYCAAYETLVAAAGCGASPD 287
QY 100 YGGVTVQEPYGNKLLQGGYAAHYAQPTPATAAYSDSYGRVYAADPYHHTLAPAPYQ 159
Db 288 YNSSEYEGPLSPPLCLNGNFSLMQDSSPDHEKSYHVS-----MHYSGCPGSRHG 336
QY 160 VG 161
Db 337 HG 338

Search completed: January 15, 2004, 08:41:50
Job time : 50 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2004, 08:51:30 ; Search time 263.148 Seconds
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2719.103 Million cell updates/sec

Title: US-09-809-545A-2
Perfect score: 1086
Sequence: 1 MTNKKAVNPFYNGMKLNPV.....VLSSLDASTYGGYNNFAPY 203

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Delop 6.0 , Delext 7.0

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1086	100.0	1340	10	US-09-809-545A-1	Sequence 1, Appli
2	955	87.9	2372	9	US-09-794-591-1	Sequence 1, Appli
3	519	47.8	1558	13	US-10-094-749-287	Sequence 287, App
4	500.5	46.1	1843	11	US-09-919-039-266	Sequence 266, App
5	467.5	43.0	1506	13	US-10-359-385-5	Sequence 5, Appli
6	231.5	21.3	2397	12	US-10-104-047-559	Sequence 65, App
7	116	10.7	11447	13	US-10-301-822-55	Sequence 25, Appli
8	116	10.7	11447	15	US-10-177-293-60	Sequence 60, Appli
9	116	10.7	11560	15	US-10-177-293-62	Sequence 62, Appli
10	116	10.7	11657	15	US-10-198-846-11039	Sequence 11039, A
11	108.5	10.0	6830	14	US-10-098-841-226	Sequence 226, App
12	107	9.9	895	9	US-09-770-445-481	Sequence 481, App
13	103	9.5	7053	13	US-10-252-157-219	Sequence 219, App
14	102.5	9.4	1089	15	US-10-156-761-1655	Sequence 2655, App
15	102.5	9.4	9025608	15	US-10-156-761-1	Sequence 1, Appli
16	99.5	9.2	5643	13	US-10-012-952A-43	Sequence 43, Appli
17	99	9.1	60	13	US-09-908-975-7420	Sequence 7420, Ap
18	99	9.1	464	13	US-10-027-632-18118	Sequence 18118, A
19	99	9.1	464	14	US-10-027-632-18118	Sequence 18118, A
20	98.5	9.1	821	10	US-09-996-634-62	Sequence 62, Appli
21	98.5	9.1	821	11	US-09-997-182-62	Sequence 62, Appli
22	98.5	9.1	821	11	US-09-997-181-62	Sequence 62, Appli
23	97.5	9.0	2658	9	US-09-815-242-4035	Sequence 4035, Ap
24	97.5	9.0	3285	10	US-09-712-363-143	Sequence 143, App
25	96	8.8	1380	12	US-10-369-493-31940	Sequence 31940, A
26	96	8.8	1380	8	US-08-754-311B-1	Sequence 1, Appli
27	95.5	8.8	599	13	US-10-029-386-20712	Sequence 20712, A
28	95.5	8.8	1317	12	US-10-369-483-11645	Sequence 31645, A
29	95.5	8.8	9025608	15	US-10-156-761-1	Sequence 1, Appli
30	94.5	8.7	389	13	US-10-029-386-13913	Sequence 13913, A
31	94.5	8.7	563	13	US-10-029-386-206	Sequence 206, App
32	94.5	8.7	3044	12	US-10-108-260A-2049	Sequence 2049, App
33	94	8.7	657	10	US-09-974-300-1655	Sequence 1655, App
34	93.5	8.6	594	13	US-10-120-988-71	Sequence 71, Appli
35	93	8.6	2076	15	US-10-156-761-7099	Sequence 7099, App
36	92.5	8.5	699	13	US-10-027-632-24830	Sequence 24830, A
37	92.5	8.5	699	13	US-10-027-632-24831	Sequence 24831, A
38	92.5	8.5	699	13	US-10-027-632-24832	Sequence 24832, A
39	92.5	8.5	699	14	US-10-027-632-24830	Sequence 24830, A
40	92.5	8.5	699	14	US-10-027-632-24831	Sequence 24831, A
41	92.5	8.5	699	14	US-10-027-632-24832	Sequence 24832, A
42	92.5	8.5	1622	13	US-10-029-386-22666	Sequence 22666, A
43	92.5	8.5	2273	10	US-09-822-830A-410	Sequence 410, App
44	92.5	8.5	2390	10	US-09-880-107-3769	Sequence 3769, App
45	92.5	8.5	2390	13	US-09-873-319-717	Sequence 717, App

ALIGNMENTS

RESULT 1
US-09-809-545A-1
Sequence 1, Application US/09809545A
Patent No. US20020110804A1
GENERAL INFORMATION:
APPLICANT: Stanton, Lawrence W.
TITLE OF INVENTION: SECRETED FACTORS
FILE REFERENCE: SCIOS.017A
CURRENT APPLICATION NUMBER: US/09/809,545A
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1340
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-809-545A-1

Alignment Scores:
Pred. No.: 1,82e-118
Score: 1086.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Length: 1340
Matches: 203
Conservative: 0
Mismatch: 0

Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-809-545A-2 (1-203) x US-09-809-545A-1 (1-1340)

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Db      535 ATGACATAATAAAAGCCGCGTGAACCCCTACCAAGGCTGGAAATTAATTCAGTTGTG 594

Qy      21 GYALAVAlTySerProaAspPheTyAlaGlyThrValLeuLeuCyseGlnAlaAsnGln 40
Db      595 GGCACCGGTCTACACACCCCGACTTCTATGACAGCAGCGGTGCTGTCAGGCGCAACAG 654

Qy      41 GlnGlySerSerMetTySerGlyProSerSerLeuValTyThrSerAlaMetProGly 60
Db      655 GAGGAGCTTCTCATGTACAGTGGCCCAAGTTCACTTGTATTAATCTTTCAGATCCCTGGC 714

Qy      61 PheProTyProAlaAlaThrAlaAlaAlaAlaTyArgGlyAlaHisLeuArgGlyArg 80
Db      715 TTTCATATCCGCGCGCACCTGTCAGAGCTGCATACGAGGAGGCTCACCTTCAGAGCGCT 774

Qy      81 GYARgThrValTyRanThrPheArgAlaAlaAlaAlaProPProPProIleProAlaTy 100
Db      775 GGTGCACCGGTACAAACACCTTCAGAGCTGCGCGCGCCGCCCAATCCCGCCTAT 834

Qy      101 GYVAlValValTyRngInlProValTyRgYsAsnYsLeuLeuGlnGlyTyAla 120
Db      835 GCGGAGTAGTGTATCAAGACCGAGTATAGCAATTAATTCATACAGGAGTTCAGCT 894

Qy      121 AlaTyArgTyAlaGlnProThrProAlaThrAlaAlaTySerAspSerTyGly 140
Db      895 GCATACCGCTACGCGCACGCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 954

Qy      141 ArgValTyAlaAlaAspProTyHisHisThrLeuAlaProAlaProThrTyGlyVal 160
Db      955 CGAGTTATGTCTCGACCCCTACACACCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1014

Qy      161 GYAlaMetAsnAlaPheAlaProLeuThrAspAlaTyRgSerHisAlaAspAsp 180
Db      1015 GGTCCCATGATGCTTTTGGCCCTTTCAGCATGCCAAGACTAGAGCCATGCTGATGAT 1074

Qy      181 ValGlyLeuValLeuSerSerLeuGlnAlaSerIleTyRngInlGlyTyRAsnArgPhe 200
Db      1075 GTGGGTCTCGTTCTTTCTTCTTCTGACGCTAGTATATACCAAGGGGATACACCGTTT 1134

Qy      201 AlaProTyR 203
Db      1135 GCTCCATAT 1143

```

RESULT 2

```

US-09-794-591-1
; Sequence 1, Application US/09794591
; Patent No. US20010018198A1
; GENERAL INFORMATION:
; APPLICANT: Pulac, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins.
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/794,591
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/145,391
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (987) .. (1979)
; US-09-794-591-1

```

Alignment Scores:

Pred. No.:	1,136-102	Length:	2372
Score:	955.00	Matches:	189
Percent Similarity:	86.94%	Mismatches:	4
Best Local Similarity:	85.14%	Indels:	21
Query Match:	87.94%	Gaps:	2

US-09-809-545A-2 (1-203) x US-09-794-591-1 (1-2372)

```

Qy      1 MetThAsnlybYsAlaValaAsnProTyThrAsnGlyTrpYsLeuAsnProValVal 20
Db      1572 ATGACAAATATAAAAGCCGCGTGAACCCCTACCAAGGCTGGAAATTAATTCAGTTGTG 1631

Qy      21 GYALAVAlTySerProaAspPheTyAlaGlyThrValLeuLeuCyseGlnAlaAsnGln 40
Db      1632 GGTGAGTCTTACAGTCCCGAATCTTATGACAGCAGTCTGTTGTGCGAGCCACAG 1691

Qy      41 GlnGlySerSerMetTySerGlyProSerSerLeuValTyThrSerAlaMetProGly 60
Db      1692 GAGGAGTCTTCTCATGTACAGTGGCCCAAGTTCACTTGTATTAATCTTTCAGATCCCTGGC 1751

Qy      61 PheProTyProAlaAlaThrAlaAlaAlaAlaTyArgGlyAlaHisLeuArgGlyArg 80
Db      1752 TTCCCGATCCAGACAGCACCGCGCGCGCTTACCGAGGCGCACCTGCGAGGCGCGC 1811

Qy      81 GYARgThrValTyRanThrPheArgAlaAlaAlaAlaProPProPProIleProAlaTy 100
Db      1812 GGTGCACCGGTACAAACACCTTCAGAGCTGCGCGCGCCGCCCGCCCGATCCGCGCTTAC 1871

Qy      101 GYVAlValValTyRngInlProValTyRgYsAsnYsLeuLeuGlnGlyTyAla 120
Db      1872 GCGGAGTGTCTTACCAAGATGATGATTTATGTGACAGC-ATTATAGTGTGATATGC 1928

Qy      120 AlaTyArgTyAlaGlnProThrProAlaThrAlaAlaTySerAspSer----- 138
Db      1929 TGCATACCGGTACGCGCACGCTACCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1987

Qy      139 ----- 142
Db      1988 AGTTCGCTCTTTCGACGACGATGAATTTCTTGTACACCTTCGACGATTCAGGACAGT 2047

Qy      142 TYAlaAlaAspProTyHisHisThrLeuAlaProAlaProThrTyRgYsAlaGlyAl 162
Db      2048 TTATGCTGCGGACCCCTACACACGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2107

Qy      162 aMetAsnAlaPheAlaProLeuThrAspAlaTyThrArgSerHisAlaAspValGly 182
Db      2108 CATGAATGCTTTGACACCTTGACTGATGCAAGACTAGAGGACATGCTGATGATGAGG 2167

Qy      182 YLeuValLeuSerSerLeuGlnAlaSerIleTyRngInlGlyTyRAsnArgPheAlaP 202
Db      2168 TCTGCTCTTCTTCTTCTTCTGACGAGCTGATATATACCGAGGGGATACACCGCTTTGCTCC 2227

Qy      202 OTYR 203
Db      2228 ATAC 2231

```

RESULT 3

```

US-10-094-749-287
; Sequence 287, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI

```

APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKI, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOFUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 287
LENGTH: 1558
TYPE: DNA
ORGANISM: Homo sapiens
US-10-094-749-287

Alignment Scores:
Pred. No.: 2,04e-51 Length: 1558
Score: 519.00 Matches: 119
Percent Similarity: 59.64% Conservative: 14
Best Local Similarity: 53.36% Mismatches: 39
Query Match: 47.79% Indels: 52
DB: 13 Gaps: 8

US-09-809-545a-2 (1-203) x US-10-094-749-287 (1-1558)

QY 1 MetThrAsnLysLysAlaValAsnProGlyTrpLysLeuAsnProValVal 20
DB 854 ATGACCAATGAAGATGTCACACCATATGCAAAATGTTGAATAATACCCAGTAGTT 913
QY 21 GValAlaValTyrSerProAspPheTyrAla 30
DB 914 GAGCGTGTATATGCTCCGAGTATATATGACATTCAGCTTCAAGCAGATGTGCTCTTA 973
QY 31 GValThr-ValLeuLeuGlyGlnAlaGlnGlnGlySerSerMetTyrSerGlyProse 50
DB 974 GGCATGATATGACAGAGTCCCTATCGAAGAGGGGTATCAACTTACATT-CCT-- 1030
QY 50 rSerLeuValTyrTrsSerAlaMetProGlyPheProTyrPro--AlaAlaThrAlaAl 69
DB 1031 ---TTATCATGCTCCCTTATGTTCTGCTTCCCTTACCTTACCTATGACGACCAAGCGC 1086
QY 69 aAlaAlaTyrArgGlyAlaHisLeuArgGlyArgGlyValTyrValTyrAsnThrPheAr 89
DB 1087 AGCGCGCTTTCAGAGAGCCCATTTGAGGGGCGACAGGGCGAGCATATATGTCAGTCCG 1146
QY 89 gAlaAlaAlaProProProProProProProProProProProProProProProProPro 109
DB 1147 A--GGCGTACCTTCCACAGCCATCCCGCTTACAGGTGCTTACCAAGAGCGGATT 1203
QY 109 lTyrGlyAsnLysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrPr 129
DB 1204 TTAAGGCTGCTGAC---CTTATGCTGATATGACAGCTTACAGATATGACAGCTGCTAC 1260
QY 129 cAlaThr-----AlaAlaAlaTyrSerAspSerTyrGlyAr 141
DB 1261 TGAACCGCAGCAGCCGCTGTCAGCCGCTGACGCGCTTACGATGACGCTTATGCGAG 1320
QY 141 gValTyrAlaAlaAspProTyrHisThrLeuAlaProAlaProThrTyrGlyValG 161
DB 1321 GGCTATACAGCGGACCCCTAC---CATGCCCTTGCCCTGCGCTACGATATGAGATTGG 1377
QY 161 yAlaMetAsnAlaPheAlaProLeuThrAspAlaValTyrArgSerHisAlaAspAspVa 181
DB 181 yAlaMetAsnAlaPheAlaProLeuThrAspAlaValTyrArgSerHisAlaAspAspVa 181

DB 1378 CGCTGTG----- 1384
QY 181 lGlyLeuValLeuSerSerLeuGlnAlaSerIleTyrGlnGlyTyrAsnArgPheAl 201
DB 1385 -----CGAGTTTATACCAAGGTGCTTACAGCGGATTTCG 1419
QY 201 aProTyr 203
DB 1420 CCCCTAC 1426

RESULT 4

US-09-919-039-266
Sequence 266, Application US/09919039
Publication No. US20030108871A1
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 266
LENGTH: 1843
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: Incyte ID No. US20030108871A1 253783.3
FEATURE:
NAME/KEY: unsure
LOCATION: 1824
OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-266

Alignment Scores:
Pred. No.: 3.89e-49 Length: 1843
Score: 500.50 Matches: 105
Percent Similarity: 52.61% Conservative: 6
Best Local Similarity: 49.76% Mismatches: 23
Query Match: 46.09% Indels: 77
DB: 11 Gaps: 5

US-09-809-545a-2 (1-203) x US-09-919-039-266 (1-1843)

QY 1 MetThrAsnLysLysAlaValAsnProGlyTrpLysLeuAsnProValVal 20
DB 1228 ATGACCAACAAAGAAAGCGGGAACCCCTACACCAAGCGCTGGAAGCTAATCCAGTGTCTC 1287
QY 21 GValAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuGlyGlnAlaGln 40
DB 1288 GCGCGAGTCTTACAGGGCGTGAATTTATATGACAGTACG- 1323
QY 41 GlnGlySerSerMetTyrSerGlyProSerSerLeuValTyrTrsSerAlaMetProGly 60
DB 1324 -----GGG 1326
QY 61 PheProTyrProAlaAlaThrAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 80
DB 1327 TTCCTTACCCACCAACGCGGACAGCGCTGCTACCGGGGCGCACATCTTCCGGGCGCG 1386
QY 81 GlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProProProProProProPro 100
DB 1387 GCGCGGCGGTATATATATATTTGGGCTGGCGCACCCCGACCCCGCATCCGACTTAC 1446
QY 101 GlnGly----- 102
DB 1447 GAGCGGACACTGAGCAAAAGCTTGTAAATGCCAGTCCCATGGGCGGCGCTGGCACCG 1506
QY 102 ----- 102

```

Db      1507 TGCCCCCTCCCTCCTCAGACAGACCGAGCCGCTACCCACCTCTCCAGCGCTTCCA 1566
Qy      103 -----ValValTyrGlnGluProValTyrGlyAsnLys 113
Db      1567 CCACCTTCTGTCGCGTTTGCTTCCAGGAGTCTGTATCAGATGAGATTATTGGTCTGAG 1626
Qy      114 LeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThrAlaAla 133
      1627 ---ATTATGAGAGCTACGACGCTTACAGATAGCTCAGCCCGCT---GCAGCGCGGCA 1680
Db      134 AlaTyrSerAspSerTyrGlyArgValTyr---AlaAlaAspProTyrHisLeu 152
      1681 GCCTACAGCAGCAGATTACGAGAGCTACGACGCTCCGACCGCTACATCAGCAGCATC 1740
Qy      153 AlaProAlaProThrTyrGlyValGlyAlaMet 163
Db      1741 GGGCCCGCGGACCTTACAGCATTGGAAACCATG 1773

```

RESULT 5

```

US-10-359-385-5
; Sequence 5, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; PRIORITY FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 1250374
US-10-359-385-5

```

```

Alignment Scores:
Pred. No.: 2,37e-45 Length: 1506
Score: 467.50 Matches: 107
Percent Similarity: 56.48% Conservative: 15
Best Local Similarity: 49.54% Mismatches: 39
Query Match: 43.05% Indels: 56
DB: 13 Gaps: 8

```

US-09-809-545A-2 (1-203) x US-10-359-385-5 (1-1506)

```

Qy      1 MetThrAsnLysValAlaValAsnProTyrThrAsnGlyTyrLysLeuAsnProValVal 20
      768 ATGACCAATAGAGAGATGCTACACCATATCAATGCTTGAATTAAGCCGCTAGT 827
Qy      21 G1yAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCySglnAlaAsn--- 39
      828 GGAAGCTGATATGTCGCGAGTATATGACATCCAGCTTCAAGAGATGTCTCCTTA 887
Qy      40 ---GlnGlnGlySerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
      888 GGCATATGATGACAGTCCCTCATCAGGAAGAGGGGTATCAACACTTACATTCCTTTA 947
Qy      57 AlaMetProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaTyrArgGlyAla 75
      948 ATCATCTCTGCGCTTCCCTTACCTTACCTGACAGCCACGAGGAGCGCTTCAAGAGACC 1007
Qy      76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProPro 95

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```

Db      1008 CATTTGAGGGGAGAGGGGGAGAGATATATGTGACGTCCGA---GCGTACCTCCAAACA 1064
Qy      96 ProIleProAlaTyrGlyGlyValValTyrGlnGluProValTyrGlyAsnLysLeu 115
Db      1065 GCATCTCCCGCCCTATCC----- 1081
Qy      116 GlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
      1082 AGGGGTGATATGACACTTACAGATATGACAGACGCTCTACTCCAAACCGAGCCGCT 1141
Qy      132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
      1142 GCTGACCGCGCTGACCGCTTACAGATGAGGTATGAGGAGGTGTACACAGCGGACCC 1201
Qy      148 TyrHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla 167
      1202 TAC---CATGCCCTTGCCTCGCGCTGAGTATGAGATTGGCGCTGTG----- 1246
Qy      168 ProLeuThrAspAlaTyrThrArgSerHisAlaAspAspValGlyLeuValLeuSerSer 187
      1246 ----- 1246
Qy      188 LeuGlnAlaSerIleTyrGlnGlyGlyTyrAsnArgPheAlaProTyr 203
      1247 -----GCGATTATATCCGAGGTGGCTACAGCCGATTGGCCCCCTTAC 1288

```

RESULT 6

```

US-10-104-047-659
; Sequence 659, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1 full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; PRIORITY FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 659
; LENGTH: 2397
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-104-047-659

```

```

Alignment Scores:
Pred. No.: 3,22e-17 Length: 2397
Score: 231.50 Matches: 51
Percent Similarity: 57.00% Conservative: 6
Best Local Similarity: 51.00% Mismatches: 8
Query Match: 21.32% Indels: 35
DB: 12 Gaps: 3

```

US-09-809-545A-2 (1-203) x US-10-104-047-659 (1-2397)

```

Qy      112 AsnLysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
      2058 TCTTCTCTCTGTATGAGGTGATATGACGCTTACAGATATACAGACCTGTACTGCAAC 2117
Qy      132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyr 143
      2118 GCAAGCACCGCTGTGACGCGCTGACGCGCTTACAGTACGATATGACAGGGGTGTAC 2177
Qy      144 AlaAlaAspProTyrHisThrLeuAlaProAlaProThrTyrGlyValGlyAlaMet 163
      2178 ACAGCCGACCCCTTAC---CATGCCCTTGCCTCGCGCTGAGTATGAGATTGGCGCTGTG 2234
Qy      164 AsnAlaPheAlaProLeuThrAspAlaTyrThrArgSerHisAlaAspAspValGlyLeu 183
      2234 ----- 2234
Qy      184 ValLeuSerSerLeuGlnAlaSerIleTyrGlnGlyGlyTyrAsnArgPheAlaProTyr 203

```

[illegible]

```

QY      150 |||||-----ProleuthrAspAlalysThArgSerHisAlaspaVal 167
DB      6514 CACAACTCAATCCAGCACACCCTTGCAGATGATGTCGATGTTAATCTTATGCTCAATT 6564
QY      168 -----ProleuthrAspAlalysThArgSerHisAlaspaVal 181
DB      6565 GATTCGTGACTACGTGCCCCCTTGACAGATCAGCGACTACA----- 6606
QY      182 GlyLeuValIeuSerSerLeuGlnAlaSerIleTyrgLgylTyrsanRgpHe 200
DB      6607 ---TTATATTATAATGAATGAACAGATCTGAAAATTACAGATGGGTGGATACATTCC 6660

RESULT 8
US-10-177-293-60
; Sequence 60, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Ganmavaru, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bat Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Puzetai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegül
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
; FILE REFERENCE: MRI -038
; CURRENT APPLICATION NUMBER: US/10/177,293
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-60

Alignment Scores:
Pred. No.:          0.0107           Length:       11447
Score:             116.00           Matches:        45
Percent Similarity: 34.08%         Mismatches:     16
Best Local Similarity: 25.14%      Indels:         54
Query Match:       10.68%          Gaps:           64
DB:                15              Gaps:           8

US-09-809-545A-2 (1-203) x US-10-177-293-60 (1-11447)
QY      50 SerSerIeuValIyrThrSerAlaMetProGlyPheProTyrrProAlaIarPhAla 69
DB      6232 AACCAATTAATTCGACGCCCTGCAACCTGCACACTCCATTA---AAATTACTGTATT 6288

```

Qy	70	AlaIalaTyraG-----GlyAlaHisLeuArgGlyValGlyArgGlyThVal-----	84
Db	6289	GCTGTTTATGAAGATGAGATGAGTGCGCATCTTAACAGGAATAATGAGAGAACTGTGGACTC	6348
Qy	85	-----TyrAsnThrPheArgAlaIalaIa 92	
Db	6349	CTTCCTCCTCAGAACATGACATCTCTGACGAATGGTGTATACAGATTTTCAGGGGTCTCCG	6408
Qy	93	ProProProProlIleProIalaTyGlyGlyValValTyGlnGlnProValTyGlyAsn 112	
Db	6409	GATCCTTCACCTTCTCCAGTTCTTGGAATATAAATAGTATATAAAGCCAGTGGTTCAT	6468
Qy	113	LysLeuLeuGln-----GlyGlyTyraIalaIaTyraGlyTyraGlnProThrPro 129	
		:::	
Db	6469	GAGCCCATGGAAGCCTTGTGTGAGAAATGACATCATATACCTTA-----	6513
Qy	130	AlaThrIalaIalaIaTySerThrSerProTyGlyArgValTyraIalaIaSerProTyHis 149	
Db	6513	-----	6513
Qy	150	HisThrLeuAlaProIalaProThrTyGlyValGlyAlaMetAsnAlaPheAla-----	167
Db	6514	CACAAATCTCAATCCAGACACCACTCAACATGTG-----AAAGTTTAATGCTCAAAAT	6564
Qy	168	-----ProLeuThrAspAlaIaTySerThrArgSerHisAlaAspAspVal 181	
Db	6565	GATTTCGACTCAGATGTCCCTCTGCACATCAAGCACTACA-----	6606
Qy	182	GlyLeuValLeuSerSerLeuGlnAlaSerIleTyGlnGlyGlyTyraAsnArgPhe 200	
Db	6607	---TTATATTAAATGTACAGATGTGAAAACTTACAGATTTGGGTGGGATATACCTC 6660	

RESULT 9

US-10-177-293-62
Sequence 62, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen
APPLICANT: Zhao, Xumei
APPLICANT: Gannawarpu, Manjula
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Baer Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Puzatzi, Lajos
APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegül
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT
FILE REFERENCE: MRI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14

```

: NUMBER OF SEQ ID NOS: 506
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 62
: LENGTH: 11560
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: 10981
: OTHER INFORMATION: n = A,T,C or G
US-10-177-293-62

Alignment Scores:
Pred. No.:          0.0108      Length:      11560
Score:              116.00      Matches:     45
Percent Similarity: 34.08%      Conservative: 16
Best Local Similarity: 25.14%    Mismatches:  54
Query Match:        10.68%      Indels:     64
OB:                  15          Gaps:         8

```

US-09-809-545A-2 (1-203) X US-10-177-293-62 (1-11560)

Oy	50	SerSerIleValIYrThrnservalameProdiYhePcoYrProalalThrIala	69
Dd	6345	AACAAATGAATACCTGCAGCCCCCTGCAACTGAACTCCATATT---	6400
Oy	70	AlaAlaIyrArg-----GlyAlaHisLeudargIylarGlyArgThval-----	84
Dd	6402	GCTGTTTATGAGAATGGAGATGTGCCCATCTTAAACGGAAATGGAGAAGACTGTGGACTC	6466
Oy	85	-----TyraenthrPheaargAlaIala	92
Dd	6462	CTTCCTCCTCGAACAATACATCTCTGCAGATGGTATTAACAAGATTCAGGGTGCTCGG	6521

?

Qy	113	lysleuLeuGln-----GlyGlyTyralaalaTyraGlyTalaGlnProthPro	129
Db	6582	GATCCTTCACCTTCTCCAGTTCTTGGAATATAAATAGATATTAAGCCAGTGGTCCAA	6588
Qy	6582	GAGCCCATCGAAGACCTTGTGGAGAAATGACATCATATACCTTA-----	6622
Db	130	AlaThrAlaAlaAlaTySerAspSerTyTalaGValTyTAlaAlaAspProTyhis	149
Qy	6626	-----	6622
Qy	150	HisThrLeuAlaProAlaProThrTyTyrGlyValGlyAlaMetAsnAlaPheAla-----	167
Db	6627	CACAATTCATCAATCCAGACACCACTTACGATGTG-----AAAGTTTATCTCATAT	6677
Qy	168	-----ProLeuThrAspAlaTySerThrArgSerHisAlaAspAspVal	181
Db	6678	GATCTGGACTCAGTGTCCCTTCGACAGATCAAGCACTTACA-----	6713
Qy	182	GlyLeuValLeuSerSerLeuGlnAlaSerLeuTyGlnGlyGlyTyTyrAsnArgPhe	200
Db	6720	---TTAATATTTAAATTAACAGATCTGAAAATTACCAAGATTGGGTGGGATACATTC	6773

RESULT

```

US-10-198-846-11039
? Sequence 11039, Application US/10198846
? Publication No. US2003009974A1
? GENERAL INFORMATION:
? APPLICANT: Lillie, James
? APPLICANT: Xu, Yongyao
? APPLICANT: Wang, Youzhen
? APPLICANT: Steilmann, Kathleen
? TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
? TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, AND
? TITLE OF INVENTION: THERAPY OF BREAST CANCER
? FILE REFERENCE: MRI-049
? CURRENT APPLICATION NUMBER: US/10/198,846
? CURRENT FILING DATE: 2002-07-18

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PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FASTSEQ For Windows Version 4.0
SEQ ID NO 11039
LENGTH: 11657
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1, 2, 3, 4, 11656, 11657
OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11039

Alignment Scores:
Pred. No.: 0.0109 Length: 11657
Score: 116.00 Matches: 45
Percent Similarity: 34.08% Conservative: 16
Best Local Similarity: 25.14% Mismatches: 54
Query Match: 10.68% Indels: 64
DB: 15 Gaps: 8

US-09-809-545A-2 (1-203) x US-10-198-846-11039 (1-11657)

Qy 50 SerSerLeuValIYrThrSerAlaMetProGlyPheProTYrProAlaAlaThrAla 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6398 AACATGTAAATATCTGCAGCCCTCGACACTGACACTCATAT--AAATATCTGTTATT 6454
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 70 AlaAlaIYrArg-----GlyAlaHisLeuArgGlyArgGlyArgThrVal----- 84
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6455 GCTGTTTATGAAGATGAGATGGTGGCCATCTTACACGAAATGAAAGAACTGTGGACTC 6514
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 85 -----TyrAenThrPheArgAlaAlaAla 92
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6515 CTTCCTCCTCAGAACATACATCTCTGACGAATGATATACAAATTCAGGGTGTCTGG 6574
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 93 ProProProProlleProAlaIYrGlyIYrGlnIYrGlnIYrGlnIYrGlnIYrGlyAsn 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6575 GATCCTTCACCTTCTTCAGTTCTTGGAATATAAAGATATATAGCCAGTGGTCCAAAT 6634
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 113 LysLeuLeuGln-----GlyGlyTyrAlaAlaIYrArgTYrAlaGlnProThrPro 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6635 GAGCCCATGGAAGCCTTTGTTGGAGAAATGACATCATATACCTTA----- 6679
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 130 AlaThrAlaAlaAlaIYrSerAspSerTYrGlyArgValTYrAlaAlaAspProTYrHis 149
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6679 ----- 6679

Qy 150 HisThrIleuAlaProAlaProThrTYrGlyValGlyAlaMetAsnAlaPheAla----- 167
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6680 CACAAATCATATCCACGACACCACTCACATATG-----AATGTTATAGCTCAATAT 6730
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 168 -----ProLeuThrAspAlaIYrThrArgSerHisAlaAspAspVal 181
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6731 GATTCTGACACTCAAGTGTCCCTCTGACAAATCAAGGCACTTACA----- 6772
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 182 GlyLeuValIleuSerSerLeuGlnAlaSerIleTYrGlnIYrGlyTYrAsnArgPhe 200
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6773 ---TTATATTTAATGTAACAGATCTGAAGAAACTTACAGATTTGGGTGGATATATTC 6826
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-10-098-841-226
Sequence 226, Application US/10098841
Publication No. US20020197679A1
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, DianRui
APPLICANT: Zhao, Qing A.

```

[illegible]

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Db 702 ---GTTGATGCTGCCGACCTCATGTCACACACAGGTCGTCCAGCCCAAC--- 755
|||
Qy 159 G1yValG1yAlaMetAlaPheAlaProLeuThrAspAlaIleYrThrArgSerHisAla 178
|||
Db 756 -----AGCATTCCTCTGCTATCTTACCCAGCACCTTGTGCGCCGAGAGACCAACGCT 809
|||
Qy 179 AspApeValG1yLeuValIleuSerSerLeuGlnAla 190
|||
Db 810 GTGCCCATGGGCAATGGTCAGCAGCACCAACCATGGCA 845

RESULT 12
US-09-770-445-481/C
; Sequence 481, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Goflach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Moessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricke, Maia
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hubban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: PaedSeq for Windows Version 4.0
; SEQ ID NO 481
; LENGTH: 895
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-481

Alignment Scores:
Pred. No.: 0.00456 Length: 895
Score: 107.00 Matches: 52
Percent Similarity: 36.60% Conservative: 19
Best Local Similarity: 26.80% Mismatches: 63
Query Match: 9.85% Indels: 60
DB: 9 Gaps: 11

US-09-809-545A-2 (1-203) x US-09-770-445-481 (1-895)
Qy 42 G1ySerSerMetYrSerG1yProSerSerLeuValYrThrSerAlaMetProG1yPhe 61
|||
Db 869 GGTATGTCCTTACCAAGTCCA-----ACACGACGACGACCGTCATAT 825
|||
Qy 62 ---ProYrProAlaIle-----ThraAlaIleAlaIleYrArgG1yAla 75
|||
Db 824 GATTCAACACGACGACGATCGTATGTTCACTCAGACGACCATCGTATGTTCA 765
|||
Qy 76 HisLeuArgG1yArg-----G1yArgThrValYr 85
|||
Db 764 AACCTGGCTCAACACACCAATATGTTATGATCATCAAGTGGCTTACTACCAAACTTAT 705
|||
Qy 86 AsnThrPheArgAlaIleAlaIlePro-----ProProProIle 97
```

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Db 704 CCTTCATATAGCTCTCAGACACCATCTGATGTTATATGTAACAACCCACGACGATT 645
|||
Qy 98 ---ProAlaYr-----G1yG1yValYrG1yGlnPro 108
|||
Db 644 GCCCCAGCTTATAGACGACGACGCTGCTCAGCCAGCTTCGTGTGTAACAAACTTCAGT 585
|||
Qy 109 ValYrG1yAsnYrLeuLeuGlnG1yYrYrAlaIleYrArgYrAlaGlnProThr 128
|||
Db 584 GGGTACGGGGAAGTACTCCCAACCGGTGCTATAGTTCGATCCCTCCACACGCGCGCT 525
|||
Qy 129 ProAlaThrAlaIleAlaIleYrSerApe---SerYrG1yArgValYrAlaIleApePro 147
|||
Db 524 TATGTAAATACCCCGCTCAACAGCAATGAAACTATGA-----TACATTGGCTCTCAG 471
|||
Qy 148 TyrHisHisThrLeuAlaProAlaProThrYrG1yValG1yAlaMetAsnAlaPheAla 167
|||
Db 470 TAT-----CCTAGCTATGAGAGTGGAACCATCAGCATATGCT 432
|||
Qy 168 ProLeuThrAspAlaIleYrThrArgSerHisAlaAspApeValG1yLeuValIleuSer 187
|||
Db 431 GCACCTACTGCGCAACCGCTTATTC----- 405
|||
Qy 188 LeuGlnAlaSerIleYrGlnG1yYrYrAsnArgPheAla 201
|||
Db 404 ---CAGACTGCACCTCTCTCAGCGCGCTATGACCAATCAGCA 366
|||

RESULT 13
US-10-252-157-219
; Sequence 219, Application US/10252157
; Publication No. US20030190640A1
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Pearson, Cecelia I.
; TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
; FILE REFERENCE: PA-0027-1 US
; CURRENT APPLICATION NUMBER: US/10/252,157
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/295,048
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 501
; SOFTWARE: PERL Program
; SEQ ID NO 219
; LENGTH: 7053
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030190640A1 354430.4
; NAME/KEY: unseq
; LOCATION: 727, 736, 1204, 1985-2065, 3071-3101, 6410, 6426, 6429, 6432, 6441, 6450,
; LOCATION: 6772
; OTHER INFORMATION: a, t, c, g, or other
US-10-252-157-219

Alignment Scores:
Pred. No.: 0.196 Length: 7053
Score: 103.00 Matches: 52
Percent Similarity: 36.00% Conservative: 20
Best Local Similarity: 26.00% Mismatches: 64
Query Match: 9.48% Indels: 64
DB: 13 Gaps: 11

US-09-809-545A-2 (1-203) x US-10-252-157-219 (1-7053)
Qy 18 ProValValG1yAlaValYrSerProApePhe-----TyrAlaG1y 31
|||
Db 159 CCCACCAATAGTCCAGTATAGTCTCCAGAGTTTCACTTCCTGCATTCAGCTTATGCA--- 215
|||
Qy 32 ThrValLeuLeuYrGlnAlaIleGlnG1ySer----- 44
|||
Db 216 ACTCTGCTATGAACAGCGCTGCGCACAGAACTCGTCTCTGTGCACTGAAGGACCC 275
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Qy	45	-----MetYserGlyPProSerSerLeuValTYrThnSerAlaMetProGly	60
Db	276	TTCCACCTCCCAAGTGGACACCGGAGCCGGAACCGAAGCTTACCAAGATCCTCTGGCGCT	335S
Qy	61	PheProTYrProAlaAlaThrAlaAlaAlaAlaTYrArgGlyAlaHisLeuArgGlyArg	80
Db	336	TTTCAGATAT-----ACTGGGGGACACACTTTCAG-----	365S
Qy	81	GIYArgThrValTYrAsnThrPheArgAlaAlaAlaProProProProlLeProAlaTYr	100S
Db	366	-----GTCCACCGAGCCAGAGTAACACTGCTCCACCCCTACTCCCATCCACC	416S
Qy	101	GIYGIYAlaValTYrGlnGluProValTYr-----GlyAsn	112S
Db	417	AAC-----CCTATATCAGACGGCCATGTATTCATCAGAAAGTGCCTACCCGACAGAAAT	470S
Qy	113	LyLeuLeuGlnGlnGlyTYrAlaAlaTYrArgTYrAlaGlnProThrProAlaThAla	132S
Db	471	CTGTATGCCACGGAGACCTAC-----TCACACAGCCG-----	503S
Qy	133	AlaAlaTYrSerAspSerTYrGlyArgValTYrAlaAlaAspProTYr-----HisHis	150S
Db	504	-----GTGTATGCTGCCAGCCCTCAGTATATCCACAT	536S
Qy	151	ThrLeuAlaProAlaProThrTYrGlyAlaGlyAlaMetAsnAlaPheAlaProLeuThr	170S
Db	537	ACCAAGCTCTCCAGCCCAAC-----ACATTTCCCTCTGCTATATCCAGCACT	587S
Qy	171	AspAlaTYrThrArgSerHisAlaAspArgValGlyLeuValLeuSerSerLeuGlnAla	190S
Db	588	GTTCGGCCCCGAGAGCAACAAGGTGTGCCATGGGAGCATAGTGGCAGGACGACCATGGCA	647S

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2004, 08:41:56 / Search time 67.0883 Seconds
(without alignments)
1335.564 Million cell updates/sec

Title: US-09-809-545A-2

Perfect score: 1086

Sequence: 1 MTNKKAVNPTNGMKLNPV.....VLSLSQASYYGGYNRPAY 203

Scoring table: BLOSUM62
Xgapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NOCME=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09809545 @CGN 1.133 @runat_15012004_061051_2480 -NCPUS=6 -ICPU=3
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Issued Patents_NA:*

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- 2: /cgn2_6/prodata/2/ina/5B_COMB.seq:*
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- 4: /cgn2_6/prodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	955	87.9	2372	3	US-09-145-391-1
2	467.5	43.0	1506	4	US-09-176-657-5
3	467.5	43.0	1506	4	US-09-421-299-5
4	101	9.3	914	2	US-08-935-450-10
5	98.5	9.1	821	3	US-08-990-823-62
6	98.5	9.1	821	4	US-09-477-135A-62
7	97.5	9.0	4403765	3	US-09-103-840A-2
8	97.5	9.0	4411529	3	US-09-103-840A-1
9	96	8.8	3231	1	US-08-195-152-1
10	94.5	8.7	4403765	3	US-09-103-840A-2
11	94	8.7	2368	4	US-09-343-011B-3
12	94	8.7	43280	2	US-08-804-227C-1

13	92.5	8.5	2371	2	US-08-343-443B-1	Sequence 1, Appl1
14	92.5	8.5	2412	1	US-08-437-027-18	Sequence 18, Appl1
15	92.5	8.5	28958	1	US-08-258-261B-6	Sequence 6, Appl1
16	92.5	8.5	28958	1	US-08-456-837-6	Sequence 6, Appl1
17	92.5	8.5	28958	1	US-08-457-342-6	Sequence 6, Appl1
18	92.5	8.5	28958	1	US-08-457-646A-6	Sequence 6, Appl1
19	92.5	8.5	28958	1	US-08-458-076A-6	Sequence 6, Appl1
20	92.5	8.5	28958	1	US-08-764-233A-4	Sequence 4, Appl1
21	92.5	8.5	28958	1	US-08-457-335A-6	Sequence 6, Appl1
22	92.5	8.5	28958	1	US-08-729-214-6	Sequence 6, Appl1
23	92.5	8.5	28958	3	US-09-028-934-6	Sequence 6, Appl1
24	92.5	8.5	49377	3	US-08-764-233A-1	Sequence 1, Appl1
25	92	8.5	53526	3	US-08-658-136-2	Sequence 2, Appl1
26	92	8.5	53577	3	US-08-658-136-1	Sequence 1, Appl1
27	91	8.4	1896	4	US-09-343-011B-4	Sequence 4, Appl1
28	90.5	8.3	852	4	US-09-252-991A-16108	Sequence 16108, A
29	90.5	8.3	1311	4	US-09-252-991A-16493	Sequence 16493, A
30	90.5	8.3	10095	3	US-08-822-586-45	Sequence 45, Appl1
31	90	8.3	2303	4	US-09-922-146-3	Sequence 3, Appl1
32	89.5	8.2	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
33	89	8.2	1083	4	US-09-252-991A-8817	Sequence 8817, Ap
34	89	8.2	1140	3	US-09-023-173-4	Sequence 4, Appl1
35	89	8.2	1227	4	US-09-252-991A-9232	Sequence 9232, Ap
36	89	8.2	1296	4	US-09-252-991A-9150	Sequence 9150, Ap
37	89	8.2	2715	4	US-09-252-991A-8715	Sequence 8715, Ap
38	88.5	8.1	2007	4	US-09-252-991A-3308	Sequence 3308, Ap
39	88.5	8.1	2709	4	US-09-252-991A-3326	Sequence 3326, Ap
40	88	8.1	885	4	US-09-252-991A-4426	Sequence 4426, Ap
41	88	8.1	1362	4	US-09-252-991A-4184	Sequence 4184, Ap
42	88	8.1	2923	6	5187076-5	Patent No. 5187076
43	87.5	8.1	3155	4	US-09-442-100-7	Sequence 7, Appl1
44	87.5	8.1	3155	4	US-08-939-106-7	Sequence 7, Appl1
45	87.5	8.1	44377	2	US-08-804-227C-7	Sequence 7, Appl1

ALIGNMENTS

RESULT 1
US-09-145-391-1
; Sequence 1, Application US/09145391
; Patent No. 6194171
; GENERAL INFORMATION:
; APPLICANT: Pulist, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acid Encoding Ataxin-2 Binding Proteins,
; FILE REFERENCE: CE 3093
; CURRENT APPLICATION NUMBER: US/09/145,391
; CURRENT FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (987)..(1979)
US-09-145-391-1

Alignment Scores:
Pred. No.: 2.56e-85
Score: 955.00
Percent Similarity: 86.94%
Best Local Similarity: 85.14%
Query Match: 87.94%
DB: 3
Gaps: 2

US-09-809-545A-2 (1-203) x US-09-145-391-1 (1-2372)

QY 1 MetThrAenLYeLalValaAnProTYThraNGLYTPrLYsLeuAnProValVal 20
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Db 1572 ATGACAAATTAATAAGACCGTCAACCTTATATACAAATGCGTGAATAATGACAGTTGTG 1631

Qy	21	GLYLAVALTYRSEPRQASPPHEVRLAGLYRHLAILEUQVSGNLAASGN	40
Db	1632	GGTGAGCTCAAGTCCCAAGTTCTATACAGGACGGTCTGTGTGCAAGCCAAACG	1631
Qy	41	GLUGISERSEMERLETYSERGLYPROSESERLEUVALTYRTHSERALMETPROGLY	60
Db	1692	GAGGAGTCTTCATGTATACAGTGCCCCAGTTCACTGTATATACCTTGCAATGCCAGGC	1751
Qy	61	PHPEOTLYRPROLAALATHRLAALAAALATYRAGGLYALHILEUARGLYARG	80
Db	1752	TTCCCGTATCCAGACGACCGCCGCCGCCCTTACCAAGAGGGCGACCTCGAGGCCG	1811
Qy	81	GLYARGTHVALTYRASNTHRPHEARGLAALAAALAPROPROPROGLIPEALATYR	100
Db	1812	GGTGGCACCGTGTACACACCTTCAGGGCCCGCGGCCCCCGCCGATCCCGGCTAC	1871
Qy	101	GLYGLYVALVALTYR-GINGLUPROVALTYRGLYASNLVSEUENGINGLYTYRAL	120
Db	1872	GCGCGTGTGTTATCCAGAGATGATTTTATGTGTCAGAC--ATTATGTGTGTTATGC	1928
Qy	120	AALATYRARGTYRALAGINPROTHPROALATHRLAALAAALTYSERASPSER----	138
Db	1929	TGCATACCGCTAACGCCCACTTACCCCTGCACCTGCCGTCTCAAGTGCACG-AAATC	1997
Qy	139	-----TYRGLYARGVA	142
Db	1998	AGTTGCTTTCGTTGCACAGATGAATTTCTTGTACACACCTTCGCACTTACGAGCGAGT	2047
Qy	142	ITYRLAALAAPPROTYRHLHISTHRLAUALPROALAPROTHYRGLYVALGLYAL	162
Db	2048	TTATCTCTCCGACCCCTTACCAACAGCACTTGCTTCACACCCCACTTACGCGGTGGTGC	2107
Qy	162	AMEASNALPHEALAPOLEUTHRASALALYSETHRARGSERHISLAAPAPVALGI	182
Db	2108	CATGATCTTTTGACACTTTGACTGATGACCAGACCTGAGACCACTGCTGATGATGGG	2167
Qy	182	YLEUVALLEUSERSELEUNGINALASERILEYRGLINGLYTYRASNARGPHEALAPR	202
Db	2168	TCTGCTTCTTTCTTATTGACAGCGCTAGATATACCGAGGGGATACACCGTTTGGCTCC	2227
Qy	202	OTYR 203	
Db	2228	ATAC 2231	
RESULT 2			
US-09-176-657-5			
; Sequence 5, Application US/09176657			
; Patent No. 6020164			
; GENERAL INFORMATION:			
; APPLICANT: Bandman, Olga			
; APPLICANT: Tang, Y. Tom			
; APPLICANT: Corley, Neil C.			
; APPLICANT: Guejler, Karl J.			
; APPLICANT: Lu, Aina			
; APPLICANT: Baughn, Mariah R.			
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS			
; FILE REFERENCE: PF-0611 US			
; CURRENT APPLICATION NUMBER: US/09/176,657			
; CURRENT FILING DATE: 1998-10-21			
; NUMBER OF SEQ ID NOS: 9			
; SOFTWARE: PERL Program			
; SEQ ID NO 5			
; LENGTH: 1506			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE: -			
; OTHER INFORMATION: 1250374			
US-09-176-657-5			
Alignment Scores:			
Pred. No.:	2,84e-37	Length:	1506
Score:	467.50	Matches:	107

Percent Similarity:	56.48%	Conservative:	15
Best Local Similarity:	49.54%	Mismatches:	39
Query Match:	43.05%	Indels:	56
DB:	3	Gaps:	8

US-09-809-545A-2 (1-203) x US-09-176-657-5 (1-1506)

```

QY      1 MetThrLeuValValAlaAsnProDyThrAnGlyTrpLysLeuAsnProValVal 20
DB      768 ATGACCAATAAAGAAAGATGTGTACACCAATATGCAATATGTTGAATTTAAGCCAGTATT 827
QY      21 G1ValAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCyGlnAlaAsn--- 39
DB      828 GGACCTGATATATGATCCGGAGTTATATGACGATCATCCAGCTTTCAAGCAAGATGTCTCCTTA 887
QY      40 ---GlnGluGlySerSerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
DB      888 GGCATATGATGCACAGTGCCTTCATGAGAAAGAGGGGATTCACACTTACATTCTTTTA 947
QY      57 AlaMetProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaTyrArgGlyValA 75
DB      948 ATCATTCCTGGCTTCCTTACCTACTGACGACCAACGAGCGCGCTTTGAGAGAGCC 1007
QY      76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProPro 95
DB      1008 CATTTGAGGGGCAAGGGCGGACAGTATATGTCGTACAGTCCGA---GGGATACCTCCAAACA 1064
QY      96 ProIleProAlaTyrGlyValValValTyrGlnGluProValTyrGlyAsnLysLeuLeu 115
DB      1065 GCCATCCCGCGCTATTC----- 1081
QY      116 GlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
DB      1082 AGGGGTGATATGACGCTTACAGATATGACACAGCTCTGCTACTGCACCGCAGCACCGCT 1141
QY      132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
DB      1142 GCTGACAGCGCGTGCAGCGCGCTTACAGTACCGCTTATGGCAGGGGTATCACAGCGGACCCC 1201
QY      148 TyrHisIshThrLeuAlaProAlaProThrTyrGlyValGlyAlaMetAsnAlaPheAla 167
DB      1202 TAC---CATGCCCTTGGCCCTGCGCGCTATGAGATGAGTGGCGCTGTG----- 1246
QY      168 ProLeuThrAspAlaLysThrArgSerHisAlaAspValGlyLeuValLeuSerSer 187
DB      1246 ----- 1246
QY      188 LeuGlnAlaSerIleTyrGlnGlyTyrAsnArgPheAlaProTyr 203
DB      1247 -----GGAGTTTATACCGAAGTGGCTACAGCCGATTGGCCCTTAC 1288

```

RESULT 3
US-09-421-299-5
Sequence 5, Application US/09421299
Patent No. 6524579
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Aina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT APPLICATION NUMBER: US/09/421,299
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: 09/176,657
EARLIER FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 1506
TYPE: DNA

;
; ORGANISM: Homo sapiens
;
; FEATURE: -
; OTHER INFORMATION: 1250374
US-09-421-299-5

Alignment Scores:	
Pred. No.:	2,846-37
Score:	467.50
Percent Similarity:	56.48
Best local Similarity:	49.54
Query Match:	43.05
DB:	4
Length:	1506
Matches:	107
Conservative:	15
Mismatches:	39
Indels:	56
Gaps:	8

US-09-809-545A-2 (1-203) x US-09-421-299-5 (1-1506)

Qy	1	MetThrAnuLVyLAlaValAlaAsnProTYrThrAnGlyTTPyLVLeuAsnProVal	20
Db	768	ATGACCAATACAGAAATAGTCTACACCAATATGCAAAATGGTTGAAATTAAAGCCAGTAGTT	827
Qy	21	GIAlaValTYrSerProAspPheTYrAaglTYrValLeuLeuCysGIAlaAsn---	39
Db	828	GGAGCTGATATATGCTCCGAGAGTTATATGACAGATCAGCTTCAAGCAGATGTGCCCTA	887
Qy	40	---GInGluGlySerSerMetTYrSerGlyProSerSerLeu-----ValTYrThrSer	56
Db	888	GGCAATGATGACAGCGATGCCCTTACAGAAAGGGGGATATACACTTACATTCCTTTA	947
Qy	57	AlaMetProGlyPheProTYrPro---AlaAlaThrAlaAlaAlaAlaTYrGlyVala	75
Db	948	ATCATCTCTGGCTCTCCCTTACCTTACCTGACAGCCACACGAGCGCCGTTTCAGAGAGCC	1007
Qy	76	HisLeuAArgIyAArgIyAArgThrValTYrAsnThrPheArgAlaAlaAlaProProPro	95
Db	1008	CATTGAGGGGACAGAGGGCGGACATATATGGTATGTCAGTCCGA---GCCGTACTTCACAA	1066
Qy	96	ProIleProAlaTYrGlyGlyValValTYrGInGluProValTYrGlyAsnLVLeuLeu	115
Db	1065	GCCATCCCGGCTATCC-----	1081
Qy	116	GInGlyGlyTYrAlaAlaAlaTYrArgTYrAlaGInProThrProAlaThr-----	131
Db	1082	AGGGGTGATATGCGAGCGCTTACAGATATGACACAGCTGCTACTGCAACCGCACCCGCT	1144
Qy	132	-----AlaAlaAlaTYrSerAspSerTYrGlyArgValTYrAlaAlaAspPro	147
Db	1142	GCTGACGCGCTGACGCGCTTACAGTACCGTTATGGCAGGGGTGTACACAGCCGACCC	1201
Qy	148	TYrHisThrLeuAlaAlaProAlaProThrTYrGlyValGlyAlaMetAsnAlaPheAla	167
Db	1202	TAC---CATGCGCTTGCCCTGCGCCCTGATGATGAGTTGGGGCTGTG-----	1246
Qy	168	ProLeuThrAspAlaAlaTYrThrArgSerHisAlaAspAspValGlyLeuValLeuSerSer	187
Db	1246	-----	1246
Qy	188	LeuGInAlaSerIleTYrGInGlyTYrAsnArgPheAlaProTYr	203
Db	1247	-----GGAGGTTTATACGAGGTGCTACAGCGCATTTGGCCCTTAC	1288

RESULT 4
 US-08-935-450-10
 / Sequence 10, Application US/08935450
 / Patent No. 5977311
 / GENERAL INFORMATION:
 / APPLICANT: Nandabalan, Krishnan
 / APPLICANT: Yang, Meijia
 / APPLICANT: Schulz, Vincent
 / TITLE OF INVENTION: 53BP2 COMPLEXES
 / FILE REFERENCE: 7934-054
 / CURRENT APPLICATION NUMBER: US/08/935,450
 / CURRENT FILING DATE: 1997-09-23
 / NUMBER OF SEQ ID NOS: 15
 / SOFTWARE: PatentIn Ver. 2.0

```

; SEQ ID NO 10.
; LENGTH: 914
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-935-450-10

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Alignment Scores:	
Pred. No.:	0.303
Score:	101.00
Percent Similarity:	37.06%
Best local Similarity:	28.24%
Query Match:	9.30%
DB:	2
Length:	91
Matches:	48
Conservative:	15
Mismatches:	59
Indels:	48
Gaps:	7

US-09-809-545A-2 (1-203) X US-08-935-450-10 (1-914)

Qy	2	TYTserProAspPheTyrAlaGlnThrValLeuLeuCyGlnAlaAsnGlnGlySer	43
Db	230	TACAGCCCT-----GCTGGAAACCCCCAGGGGCC	255
Qy	44	SeMetTyrSerGlyProSerSerLeuValTyrThrSerAla-MetProGlyPheProTy	63
Db	260	AGCACTTAACAATAAGAACACGAACATCTCTGGCTCAAGCGCAATATACAGACATCCCCACC	315
Qy	63	rProAlaAlaThrAla-----AlaAlaAlaTyrArgGlyAlaHisLeuAArgGlyArgG	81
Db	320	GTCAGCAGCTACAGCCCTTCCACAGCCGAGTTACGCCAGCACCTTAC--AAACAGGG	375
Qy	81	YATrGThrValTyrAsnThrPheArgAlaAlaAla-ProProProProIleProAlaTyrG	101
Db	377	GAGGTTACAGCCAGGGTTACACAGGCCACCGCTCCACCTTCACACACATCTGCTTACA	433
Qy	101	lyGlyValValTyrGlnGlnProValTyrGlyAsnlybLeuLeuGlnGlnGlyTyrAla	121
Db	437	AC-----TATGGAGC-----TACGGCGGTTACAAAC	463
Qy	121	latTyrArgTyrAlaGlnProThrProAlaThrAlaAlaAlaTyrSerAspSerTyrGly	141
Db	464	CGGCCCCCTATACCCACCGCCACCCGCCACCGCACAGACTTAC-----	507
Qy	141	rgValTyrAlaAlaAspProTyrHisHisThrLeuAlaProAlaProThrTyrGlyValG	161
Db	508	-----CCTACGCCCACTATACACAGT	528
Qy	161	lyAlaMetAsnAlaPheAlaProLeuThrAspAlaIyThrArgSerHisAlaAspArg	181
Db	530	ATCAGCAGTATCCACGAGGTGGAAACCACTACTATTCAGAACAGGGGCACT-----	575
Qy	181	alGlyLeuValLeuSerSerLeuGln	189
Db	580	--GGCGCCACTACTACGGAACTACGA	603
RESULT 5			
US-08-990-823-62			
Sequence 622, Application US/08990823D			
Patent No. 6228371			
GENERAL INFORMATION:			
APPLICANT: Nano, Francis			
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding			
FILE REFERENCE: 49086			
CURRENT APPLICATION NUMBER: US/08/990,823D			
CURRENT FILING DATE: 1997-12-15			
EARLIER APPLICATION NUMBER: US 96/10375			
EARLIER FILING DATE: 1996-06-14			
EARLIER APPLICATION NUMBER: 60/000,254			
EARLIER FILING DATE: 1995-06-15			
NUMBER OF SEQ ID NOS: 113			
SOFTWARE: Patencin Ver. 2.0			
SEQ ID NO 62			
LENGTH: 821			
TYPE: DNA			
ORGANISM: Mycobacterium tuberculosis			

QY 140 ----- GlyArgValTyrAlaIAspProTyrHis----- 150
 Db 655 GCTGGCCCTGGGGCCGCCGAGGCCGACGTGGCGG-----CATTTGCCG 699
 QY 151 -----ThrLeuAlaProAlaProThrTyrGly 159
 Db 700 CTATGACCCGAACCTGAGCCCTGAGCAATGGTTGGCTTTCAACCCCGCGGTTCCGGT 759
 QY 160 ValGlyAlaMetAsnAlaPheAlaProLeuThrAspAlaValSThrArgSerHisAlaAsp 179
 Db 760 GCTGAAATCTCTGCAGCGGTTGATGGGTTCAGCGCACACCGGTGTTGATGACATCGCGAC 819

RESULT 7
 US-09-103-840A-2
 ; Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; CURRENT FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 4403765
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; OTHER INFORMATION: CDC 1551
 ; OTHER INFORMATION: "a" bases at various positions throughout the sequence
 US-09-103-840A-2

Alignment Scores:
 Pred. No.: 6.01e+04 Length: 4403765
 Score: 97.50 Matches: 66
 Percent Similarity: 30.91% Conservative: 19
 Best Local Similarity: 24.00% Mismatches: 95
 Query Match: 8.98% Indels: 96
 DB: Gaps: 12

US-09-809-545A-2 (1-203) x US-09-103-840A-2 (1-4403765)
 QY 1 MethrAsnLysAlaValAsnProTyrThrAsnGlyTyrLysLeuAsnProValAl 20
 Db 4237678 ATGGCCGACGACGTGCTGGCCGACGCCACCCCAATGCCGGCAGTGTGCACACCGGTTCCG 4237737
 QY 21 GlyAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCysGlnAlaAsnGln 40
 Db 4237738 GACCAGCGGCTTCGACCGGACGACCGCTGAGCGGTATCAATCCCGTCCGCTTCAAAACC 4237797
 QY 41 Glu-----GlySerSerMetTyrSerGlyPro-----SerSerLeuValTyr 54
 Db 4237798 GAGGCGCGTGGCGGACGAGACTCAATGTCGACCCCGGTGCTTCCCAAAACCGCGCTGTCAAC 4237857
 QY 55 ThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaAlaTyrArgGly 74
 Db 4237858 TCCGATGCGTGGCCCAACAAACCCACCGCCCATCAACCGATCCGCGGGCACCGCGGA 4237917
 QY 75 AlaHisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaPro--- 93
 Db 4237918 -----GGAAGAGGCCCGGTGGGATCAACGGGTGCACACGCGCTGCTGCTTC 4237965
 QY 94 -----ProProProIleProAlaTyrGly----- 101
 Db 4237966 GGATTGCACCCGCGACCGTAACCCCGGTATATGGGACAGCTACGGGAGAACAACTGGCCGC 4238025
 QY 102 -----GlyValValTyrGlnGlnPro----- 108

[illegible]

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Db 4245552 GAGGGCGTGGCGGAGACCTCAAGTCCGACCCGGGTGTCTCAAAACCGGGCTGTCAAC 4245611
Qy 55 ThSer1aMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaAlaTyrArgGly 74
Db 4245612 TCCGATGCGCGCCCAACCAACCGCCGATCCGATCCGCGGGCCGCCGCGGA 4245671
Qy 75 AlAH1eUeuArgGlyArgGlyValThrValThrAsnThrPheArgAlaAlaAlaPro--- 93
Db 4245672 -----GGAGAGGCGCGGTGGGATCAACGGGTGCGACGGGGCGTCCCTTC 4245719
Qy 94 -----ProProProlleProAlaTyrGly----- 101
Db 4245720 GGAATTGACCCCGACGTAACCCGGGTATGCGAGCTACGGGAGAACCAACGTGGCCG 4245779
Qy 102 -----GlyValValTyrGlnGluPro----- 108
Db 4245780 ACGGCCACTCGCGCTGTACAGTTACCGCCCGACCGCGCGCGTGTGTG 4245839
Qy 109 -----ValTyrGlyAsn 112
Db 4245840 GTTTCGCGCGCGCGCATCTGTCTTACAGAGAGACGGCATTTTCATCTACGGCCAG 4245899
Qy 113 LysLeu---LeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
Db 4245900 TCCCTGAACCTGAGTG-GGG-----CGTCACCGCGCGGACGGCGCATCCAGCCACT 4245952
Qy 132 AlaAlaAlaTyrSerAspSerTyr----- 139
Db 4245953 GGGGCGAGTATTTCTCGATCGACATCGGACCGCAACCGCGGTGGCAATCTCGCTTCC 4246012
Qy 140 -----GlyArgValTyrAlaAlaAspProTyrHisHis- 150
Db 4246013 GCTGGCTGGGCGCGCGCGAGCGCGACGTGGCGG-----CATTTCCG 4246057
Qy 151 -----ThrLeuAlaProAlaProThrTyrGly 159
Db 4246058 CTATGACCCGAACTGAGCCCTGAGCAATGGTTCGCTTCACCGCGCGGTTCGGGT 4246117
Qy 160 ValGlyAlaMetAlaAlaPheAlaProLeuThrAspAlaThrArgSerHisAlaAsp 179
Db 4246118 GCTGGAACTCTCTCGCGGTGATCGGATCGACACCGGTGTGATGACATCGCGAC 4246177
Qy 180 AspValGlyLeuValLeuSerSerLeuGlnAlaSerIleTyrGln 194
Db 4246178 CGCAGCCAACTT-----CCCTGCGACGACCGTTTCCGA 4246213

RESULT 9
; Sequence 1, Application US/08195152
; Patent No. 5679541
; GENERAL INFORMATION:
; APPLICANT: Bonini, Nancy M.
; APPLICANT: Leiserson, William M.
; APPLICANT: Benzer, Seymour
; TITLE OF INVENTION: PROGRAMMED CELL DEATH ANTAGONIST
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohenbach, Teet, Albritton & Herbert
; STREET: 4 Embardadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,152
; FILING DATE: 14-FEB-1994

```

```

; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Treccartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-59551/RFT/RMS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3231 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; US-08-195-152-1

Alignment Scores:
Pred. No.: 5.2
Score: 96.00
Percent Similarity: 37.57%
Best Local Similarity: 24.86%
Query Match: 8.84%
DB: 1
Gaps: 6

US-09-809-545a-2 (1-203) x US-08-195-152-1 (1-3231)

Qy 42 GlySerSerMetTyr-----SerGlyProSerSerLeu 52
Db 1062 GGAATCAATTGTACGCGCTGACCTGCGCCAGCAATCCGTGACGAGAGACAGTGGCG 1121
Qy 53 ValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaTyr 72
Db 1122 GTCACTCTTCGCGCAGT-----GACGCGGACAGACGAGCGGTCTAC 1163
Qy 73 ArgGlyAlaHisLeuArgGlyArgGlyValThrValThrAsnThrPheArgAlaAla 92
Db 1164 GAGCGCAACAT-----GACTACTACTACTACACAGCATGACGAGTACAG 1211
Qy 93 ProProProProlleProAlaTyrGlyValValTyrGlnGluProValTyrGlyAsn 112
Db 1212 CCGCGCGCTTCTTACCTCCGATACGAACTCTTATCGCGCGCAACGGCGGACGCGCAG 1271
Qy 113 LysLeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThrAla 132
Db 1272 GCCAAGATGAAACCGGAGCGGAGCTGCGCGGCTGCTACTGACGCCACAGTARGCC 1331
Qy 133 AlaAla----- 134
Db 1332 GCCAGCGCAACAACTGCGAGCTGTACAGAGTCCGTACCGCGGCTACAACTTC 1391
Qy 135 -----TyrSerAspSerTyrGlyArgValTyrAlaAlaAsp 146
Db 1392 GGGCAGCAGACTACCGCGGCTACTACACAGACAGTACGCACTTATTCAGTCCGCC 1451
Qy 147 ProTyrHisThrLeuAlaProAlaPro-----ThrTyrGlyValGly--- 161
Db 1452 AACTACTACCGATGCGTACGCTGCGCGAGCTGAGTGCAGTGCATGAGCATGCTTC 1511
Qy 162 AlaMetAlaAlaPheAlaProLeuThrAspAlaThrArgSerHisAlaAspVal 181
Db 1512 CATGTGGCGCTCTCGAATCTCTCGAGAGTCCCGACGACCACTC-GACGAGGCC 1570
Qy 182 Gly 182
Db 1571 GGT 1573

RESULT 10
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.

```

APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103.840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Alignment Scores:
Pred. No.: 1.16e+05 Length: 4403765
Score: 94.50 Matches: 49
Percent Similarity: 42.26% Conservative: 22
Best Local Similarity: 29.17% Mismatches: 68
Query Match: 8.70% Indels: 31
DB: 3 Gaps: 8

US-09-809-545a-2 (1-203) x US-09-103-840A-2 (1-4403765)

QY 11 ThranglYTrpYlsuasnProvalValglYalValYserProaspPheTYrAla 30
DB 991136 ACAATGAGAGCTGTGCAATCTCTACTGCGGGGGTGGAGACT--GCATATCAG 991080
QY 31 GYrYrValleuLeuYcGlnAlaSnGlnGlnYserSerMetTYrSerGlyProser 50
DB 991079 GTGACCGGAATGCTTTGGAGCCGCGAGAAATGCCGACCTGGCCGACACATCG 991020
QY 51 Serleu-----ValTYrThrSerAlaMetProGlyPheProTYrProAlaAlaThrAla 68
DB 991019 GCGACCGGTTGCTCTACGTCATGCTGCTTGTGGCTTATTTGGCCGAGATGGGCTG 990960
QY 69 Ala-----AlaAlaTYr-ArgGlyAlaAlaHisleuArgGlyArgGly----- 81
DB 990959 GCATCTGACCGAGACCTGAGCTATCCAGGAAATCATCGGAGGCGGAGGCATCCA 990900
QY 82 -----ArgThrValTYr-----AsnThrPheArgAlaAl 91
DB 990899 ACGATGTGCGGACAAAGTTCTCGGCTATATACCAAGCCAGGTGC-TGGCGTATTGC 990841
QY 91 AlaProProProProProProProProAlaTYrGlyGlyValValTYrGlnGlnProValTYrG 111
DB 990840 GCGCCGACCGCGCGCGCCGCAATG-GCGGGGCGCTGCAATTCACGCCGCGAGGTTAGG 990782
QY 111 YAsnLYleuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 130
DB 990781 CCGG---GTGACCAAGGATGTTATGCGGCATGACGTACGCC----- 990739
QY 130 aThAlaAlaAlaTYrSerAspSerTYrGlyArgValTYrAlaAlaAspProTYrHisAl 150
DB 990738 ---GCGCTGGCGCGCGGTATGTCAGCGAGCGCTGAGGCGCAGGAGCGGCGCGCG 990683
QY 150 sThrLeuAlaProAlaProThr 157
DB 990682 ATTCTTAGGGCCGCGCGAC 990661

RESULT 11
US-09-343-011B-3
Sequence 3, Application US/09343011B
Patent No. 6306473
GENERAL INFORMATION:
APPLICANT: Stephanie Richard
TITLE OF INVENTION: SLIM-1 AND SLIM-2; NOVEL

TITLE OF INVENTION: SAM68-LIKE MAMMALIAN PROTEINS
FILE REFERENCE: A32561
CURRENT APPLICATION NUMBER: US/09/343.011B
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: CA 2265271
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 2368
TYPE: DNA
ORGANISM: Mus musculus
US-09-343-011B-3

Alignment Scores:
Pred. No.: 5.4 Length: 2368
Score: 94.00 Matches: 54
Percent Similarity: 36.93% Conservative: 11
Best Local Similarity: 30.68% Mismatches: 51
Query Match: 8.66% Indels: 60
DB: 4 Gaps: 12

US-09-809-545a-2 (1-203) x US-09-343-011B-3 (1-2368)

QY 73 ArgGlyAlaHisleuArgGlyArgGlyArgThrValTYrAsnThrPhe----- 88
DB 1673 CGGGCGGAGGTATTAGGACAGAGGAGATGAGATTAATCTCCACAGCTCATCAGAGGCG 1732
QY 89 ArgAlaAlaAlaProProProProProProAlaTYrGlyGlyValValTYrGlnGlnPro 108
DB 1733 CGTGGCGGTGCTTTCCACACACACACACACCTGAGAGAGTGTCTTACCTCG-- 1789
QY 109 ValTYrGlyAsnLYleuLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 117
DB 1790 -----GGACCACTGTGACCCGTGAGCTTTCCAGTGCCTCCATAGCAAGAGTGC 1843
QY 118 -----GlyTYrAlaAla-----TYrArgTYrAlaGlnProThr 128
DB 1844 CCACACCTGAGCCCGGGGAGCGGACAGCATACAGATACAGA--GCACCCCACT 1900
QY 129 ProAlaThrAlaAla-----AlaTYrSerAspSerTYrGlyArgValTYrAla 144
DB 1901 CCAGCTCATGATCTTATGAAATATGCTATGATGATGCTATGGGGGTGAATGAT 1960
QY 145 AlaAspProTYr-----HisHisThrleuAlaProAlaProThr----- 157
DB 1961 GACCAAGCTATAGGCTTATGATTAATAGCTACGTGACCCCAACACAAAGTGCCTGAA 2020
QY 158 -----TYrGlyValGly-----AlaMetAsnAlaPheAlaProLeuThr 170
DB 2021 TACTATGACTACGCTGATGAGTAAGAGAGATGCTTACAGACGATAGCAGACAGAAAGA 2080
QY 171 AspAlaLYleuThrArgSerHisAlaAspAspValGlyLeuValleuSerSerleuGlnAla 190
DB 2081 TGGGCAACAACCTGC-----TCCAGCTGAAAGGCA 2110
QY 191 -----SerleuTYrGlnGlnGlyTYrAsnArgPheAlaProTYr 203
DB 2111 CCACACCAAGTACGACCAAGGGGATAC--AGGAGACACCCCTAT 2155

RESULT 12
US-08-804-227C-1/C
Sequence 1, Application US/08804227C
Patent No. 5876991
GENERAL INFORMATION:
APPLICANT: Dehoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Roestek, Paul R., Jr.
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: THOMAS G. PLANT 1501

```

1 STREET: LILLY CORPORATE CENTER
2 CITY: INDIANAPOLIS
3 STATE: IN
4 COUNTRY: USA
5 ZIP: 46285
6
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM Compatible
10 OPERATING SYSTEM: MS-DOS
11 SOFTWARE: ASCII(DOS) Text only
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/804,227C
14 FILING DATE: February 21, 1997
15
16 CLASSIFICATION: 435
17 ATTORNEY/AGENT INFORMATION:
18 NAME: Plant, Thomas, G.
19 REGISTRATION NUMBER: 35,784
20 REFERENCE/DOCKET NUMBER: X-8231
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: 317-276-2459
23 INFORMATION FOR SEQ ID NO: 1:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 43280 base pairs
26 TYPE: nucleic acid
27 STRANDEDNESS: single
28 TOPOLOGY: linear
29 MOLECULE TYPE: DNA (genomic)
30
31 FEATURE:
32 NAME/KEY: CDS
33 LOCATION: 816..14234
34
35 FEATURE:
36 NAME/KEY: CDS
37 LOCATION: 14351..19945
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39 FEATURE:
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43 FEATURE:
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47 FEATURE:
48 NAME/KEY: CDS
49 LOCATION: 36249..41774
50
51 US-08-804-227C-1
52
53 Alignment Scores:
54 Pred. No.: 271 Length: 43280
55 Score: 94.00 Matches: 54
56 Percent Similarity: 40.28% Conservative: 31
57 Best Local Similarity: 25.59% Mismatches: 98
58 Query Match: 8.66% Indels: 28
59 DB: 2 Gaps: 9
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61 US-09-809-545A-2 (1-203) x US-08-804-227C-1 (1-43280)
62
63 QY 1 MetThraenlyblybAlaValaAsnProTyTrhAsnglyTrblybLeuAsnProVala1 20
64 ||| |||:::|||||::: |||::: ||| ||| |||
65 DB 8224 ATGACACACCGCGCGGCGCAGCTCGGGCGCGCGCGTCCGCGC-----GTGCGGAGCGTG 8171
66
67 QY 21 GlyAlaValaTyTrSerProAspPheTyAlaGlyTrhValLeuLeuCybGlnAlaAsnGln 40
68 ||| |||:::|||||::: |||::: ||| ||| |||
69 DB 8170 CCGGCTGGCGGTCAAGGCGCTCCCGCGCTCCGACAGG-----TCGACACAGC 8123
70
71 QY 41 GluGlySerSerMet-----TySerGlyProSerSer 51
72 ||| ||| ||| ||| ||| ||| ||| ||| |||
73 DB 8122 CGCCCGGAGCGAGTGGCGTTCGTCCCGGCGCGAAGCGCTCCAGTCGACGTCAACACACA 8063
74
75 QY 52 LeuValTyTrhSerAlaMetProGlyPheProTyTrhAlaAlaTrhAlaAlaAla 71
76 ::::: |||::: |||::: ||| ||| ||| ||| ||| |||
77 DB 8062 GTGACGACACAGCTGCTTCGTCCGACATGCGCGCCAGACGCGGTGCAAGCGCGGTG--- 8006
78
79 QY 72 TyTrAlaGlyAlaHisLeuAlaGly--ArgGlyArgThrValTyTrhValTrhPheArgAla 90
80 |||::: |||::: ||| ||| ||| ||| ||| ||| |||
81 DB 8005 -----GGGTGTCATGGCCCGGACGCCCTGCGCGGACAGATCTCTGCGCCGACCGCC 7952

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QY      91 AlaAlaProProBioProIleProAlaTyrglyglyvalValTyrglngluProValTyr 110
Db      7951 GCCATGGCTCCCGGCCCAAGGCCCCGACGCAGAGGTGCGGAGCATCCTCCGCGGCA 7892
QY      111 GlyAsnHisLeuIleuInglnglyTyrrAlaAlaTyrglytyrArgTyrAla---GlnProThrPro 129
Db      7891 CGGCGACGCTCGGCGAGGGCGTCGACCGCGCGTTGGCGGCGGCGGTACGACACTCGGCGG 7832
QY      130 AlaThrAlaAlaAlaTyrgSerAspSeryTgIyArGValTyrrAlaAlaAspPProTyrHis 149
Db      7831 GCGTTGGCCCATGTGCGCGTGACGAGAGAGAAGAGACAAGGCGTCCAACTCTTT--- 7775
QY      150 HisThrIleuAlaProAlaProThrTyrglyValGlyAlaMetAsnAlaPheAlaProIleu 169
Db      7774 -----ATGTCGCCAGCTAGTTGGTGCACAGCTCCGCGCGCACCTTCCCCCGCGG 7721
QY      170 ThrAspAlaTyrrThrArgSerHisAlaAspArgValGlyLeuValIleuSerSerLeuIn 189
Db      7720 ACGGTCTCGAAGCTC-----TCCGGTGACAGCGTGTGCATATCACCGCGTGTCCAGATTC 7667
QY      190 AlaserIleTyrgIn-----GlyIyITyr 197
Db      7666 CCGGCGGTGTGAAGACGCGCTTCCGCGGATAC 7634

RESULT 13
US-08-343-443B-1
Sequence 1, Application US/08343443B
Patent No. 5968734
GENERAL INFORMATION:
APPLICANT: Aurias, Alain
APPLICANT: Delattre, Olivier
APPLICANT: Desmazez, Chantal
APPLICANT: Melot, Thomas
APPLICANT: Peter, Martine
APPLICANT: Ploougasatel, Beatrice
APPLICANT: Thomas, Gilles
APPLICANT: Zucman, Jessica
TITLE OF INVENTION: NUCLEIC ACID CORRESPONDING TO A GENE OF
TITLE OF INVENTION: CHROMOSOME 22 INVOLVED IN RECURRENT CHROMOSOMAL
TITLE OF INVENTION: TRANSLATIONS ASSOCIATED WITH THE DEVELOPMENT OF CANCEROUS
TITLE OF INVENTION: TUMORS, AND NUCLEIC ACIDS OF FUSION RESULTING FROM SAID
NUMBER OF SEQUENCES: 129
CORRESPONDENCE ADDRESS:
ADDRESSER: Weiser & Associates
STREET: 230 South Fifteenth Street
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/06123
FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19,763
REFERENCE/DOCKET NUMBER: 989, 6121P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-875-8383
TELEFAX: 215-875-8394

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INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2371 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 25..1992
 US-08-343-443B-1

Alignment Scores:
 Pred. No.: 7.61 Length: 2371
 Score: 92.50 Matches: 48
 Percent Similarity: 33.72% Conservative: 10
 Best Local Similarity: 27.91% Mismatches: 73
 Query Match: 8.52% Indels: 41
 Gaps: 9

US-09-809-545A-2 (1-203) x US-08-343-443B-1 (1-2371)

QY	29	TYRAlAGlYThrValleuLeuCySGlnAla---AsnGlnGluGlySerSerMetYrSer	47
DB	109	TATGCACAGACCACC-----CAGGCAATATGGGCAACAAGCTATGGAACCTATGGA	159
QY	48	GLYProSerSerLeuValTYrThrSerAlaMetProGlyPheProTYrProAlaIaThr	67
DB	160	CAGCCCACTGATGTCAGCTATACCCAGGCTCAGACCACTGCACACTTATGGGAGACCGCC	219
QY	68	AlAlaIaAlaIaTYrArgGlyAlaHisLeuArgGlyArgGlyValTYrAsnThr	87
DB	220	TATGCAACTTCTTAT-----GACAGGCTCCCACTGGTTATACTACT	261
QY	88	PheArgAlaAlaIaIaProProProIleProAlaTYrGlyValValTYrGlnGlu	107
DB	262	-----CCAACTGCCCCCCAG-----GCATACAGCCAG	288
QY	108	ProValTYrGlyAsnGlyLeuLeuGlnGlyTYrAlaIaIaTYrArgTYrAlaGlnPro	127
DB	289	CCGTCCAGGGGAT-----GGCACTGCTTATGATACCACTGCT	333
QY	128	ThrProAlaThrAlaIaIaIaTYrSerAspSerTYrGlyValTYrAlaIaIaAspPro	147
DB	334	ACAGTCACCAACCCAGGCC-----TCCTATGAGCTCAGTCT	372
QY	148	TYrHisHisThrLeuAlaProAlaProThrTYrGlyValGlyAlaMetAsnAlaPheAla	167
DB	373	GCATATGCGACTCAGCTGCTTATCCAGCTATGGGCGAG-----CAG	414
QY	168	ProLeuThrAspAlaIaIaIaTYrArgSerHisAlaAspAspValGlyLeuValLeuSerSer	187
DB	415	CCAGCAGCCACTGACCTACCAAGCCGAGATGGAACAAGCCCACTGAGACTGATCA	474
QY	188	LeuGlnAlaSerIleTYrGlnGlyTYrAsnArg	199
DB	475	CCTCAATCTAGC-----ACAGGGGGTTACACACAG	504

RESULT 14
 US-08-437-027-18
 Sequence 18, Application US/08437027
 Patent No. 5670317
 GENERAL INFORMATION:
 APPLICANT: Landany, Marc
 APPLICANT: Gerald, William
 TITLE OF INVENTION: A DIAGNOSTIC TEST FOR TEST FOR THE DESMOPLASTIC
 TITLE OF INVENTION: SMALL ROUND CELL TUMOR
 NUMBER OF SEQUENCES: 21
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cooper & Dunham LLP
 STREET: 1185 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.

ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/437,027
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P
 REGISTRATION NUMBER: 28,678
 REFERENCE/DOCKET NUMBER: 46416/JPM/CCA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0525
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2412 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 US-08-437-027-18

Alignment Scores:
 Pred. No.: 7.79 Length: 2412
 Score: 92.50 Matches: 48
 Percent Similarity: 33.72% Conservative: 10
 Best Local Similarity: 27.91% Mismatches: 73
 Query Match: 8.52% Indels: 41
 Gaps: 9

US-09-809-545A-2 (1-203) x US-08-437-027-18 (1-2412)

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DB	109	TATGCACAGACCACC-----CAGGCAATATGGGCAACAAGCTATGGAACCTATGGA	159
QY	48	GLYProSerSerLeuValTYrThrSerAlaMetProGlyPheProTYrProAlaIaThr	67
DB	160	CAGCCCACTGATGTCAGCTATACCCAGGCTCAGACCACTGCACACTTATGGGAGACCGCC	219
QY	68	AlAlaIaAlaIaTYrArgGlyAlaHisLeuArgGlyArgGlyValTYrAsnThr	87
DB	220	TATGCAACTTCTTAT-----GACAGGCTCCCACTGGTTATACTACT	261
QY	88	PheArgAlaAlaIaIaProProProIleProAlaTYrGlyValValTYrGlnGlu	107
DB	262	-----CCAACTGCCCCCCAG-----GCATACAGCCAG	288
QY	108	ProValTYrGlyAsnGlyLeuLeuGlnGlyTYrAlaIaIaTYrArgTYrAlaGlnPro	127
DB	289	CCGTCCAGGGGAT-----GGCACTGCTTATGATACCACTGCT	333
QY	128	ThrProAlaThrAlaIaIaIaTYrSerAspSerTYrGlyValTYrAlaIaIaAspPro	147
DB	334	ACAGTCACCAACCCAGGCC-----TCCTATGAGCTCAGTCT	372
QY	148	TYrHisHisThrLeuAlaProAlaProThrTYrGlyValGlyAlaMetAsnAlaPheAla	167
DB	373	GCATATGCGACTCAGCTGCTTATCCAGCTATGGGCGAG-----CAG	414
QY	168	ProLeuThrAspAlaIaIaIaTYrArgSerHisAlaAspAspValGlyLeuValLeuSerSer	187
DB	415	CCAGCAGCCACTGACCTACCAAGCCGAGATGGAACAAGCCCACTGAGACTGATCA	474
QY	188	LeuGlnAlaSerIleTYrGlnGlyTYrAsnArg	199
DB	475	CCTCAATCTAGC-----ACAGGGGGTTACACACAG	504

RESULT 15

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US-08-258-261B-6
Sequence 6, Application US/08258261B
Patent No. 5639949
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip B.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/258,261B
FILING DATE: 08-JUN-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-258-261B-6
Alignment Scores:
Pred. No.: 222 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 8.52% Indels: 12
DB: 1 Gaps: 4
US-09-809-545A-2 (1-203) x US-08-258-261B-6 (1-28958)
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Db 10706 AGCGGCTCTCGACAGATGGGCATGCTTTCGCCGAGGTCCACGCCCATCCGTCCTCA 107655
QY 67 ThrAlaaIaaIaaIayr--ArgLIyAlahis-LeuArgGIyArGIyArGrThrValry 85
Db 10766 CGCTGCGCCCTCGGAGAAGACTGCGAGGCGCTCACCGCTCGATCCGTCGTCGCTCCA 108255
QY 85 rAsnThrheArGalaaIaaIaaIaPrOpPrOpPrOlePrOlaIayrGlglYyaIvalry 105
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Oy      105  rGInGluProValTyrGlyAAsnLysLeuLeuInGlyGlyTyrAlaAlaTyrAArgTyrAl 125
Db      10883 CCGGAGGCGCT-----CGCGCTCGAGTGAAGAGCATCTTCGCGCGCTTACGCTCCCC 10933
Oy      125  aGIn-----ProThrProAlaThrAlaAlaTyrSerAspSerTy 139
Db      10934 GCAGAGCTCTCCCTCCCACTTACCTTCCTCAGCGAGAGCGGTTCTGCTCGACGCTCCA 10993
Oy      139  rGlyArgValTyrAlaAlaAspPro 147
Db      10994 CGAGCGAACCGCTTCGACGCTGCGCT 11018

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Search completed: January 15, 2004, 09:58:40
Job time : 3326.09 secs

Job time : 3326.09 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2004, 08:51:30 ; Search time 191.852 Seconds
(without alignments)
2719.103 Million cell updates/sec

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Searched: 2324096 segs, 1762381658 residues
Total number of hits satisfying chosen parameters: 4648192

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	796	100.0	1340	10	US-09-809-545A-1	Sequence 1, Appl1
2	674	84.7	2372	9	US-09-794-591-1	Sequence 1, Appl1
3	441.5	55.5	1843	11	US-09-919-039-266	Sequence 266, App
4	430.5	54.1	1588	13	US-10-094-749-287	Sequence 287, App
5	379	47.6	1506	13	US-10-359-385-5	Sequence 5, Appl1
6	143	18.0	2387	12	US-10-104-047-659	Sequence 659, App
7	94	11.8	657	10	US-09-974-300-1855	Sequence 1655, App
8	92.5	11.6	699	13	US-10-027-632-24830	Sequence 24830, A
9	92.5	11.6	699	13	US-10-027-632-24831	Sequence 24831, A
10	92.5	11.6	699	13	US-10-027-632-24832	Sequence 24832, A
11	92.5	11.6	699	14	US-10-027-632-24830	Sequence 24830, A
12	92.5	11.6	699	14	US-10-027-632-24831	Sequence 24831, A
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14	92.5	11.6	11447	13	US-10-301-822-25	Sequence 25, Appl1
15	92.5	11.6	11447	15	US-10-177-293-60	Sequence 60, Appl1
16	92.5	11.6	11560	15	US-10-177-293-62	Sequence 62, Appl1
17	92.5	11.6	11657	15	US-10-198-846-11039	Sequence 11039, A
18	91	11.4	821	10	US-09-996-634-62	Sequence 62, Appl1
19	91	11.4	821	11	US-09-997-182-62	Sequence 62, Appl1
20	91	11.4	821	11	US-09-997-181-62	Sequence 62, Appl1
21	90	11.3	466	11	US-09-918-995-8298	Sequence 8298, App
22	89.5	11.2	1889	13	US-10-120-988-247	Sequence 247, App
23	89.5	11.2	3285	10	US-09-712-363-143	Sequence 143, App
24	89	11.2	1089	15	US-10-156-761-2855	Sequence 2655, App
25	89	11.2	9025608	15	US-10-156-761-1	Sequence 1, Appl1
26	87.5	11.0	2658	9	US-09-815-242-4035	Sequence 4035, App
27	87.5	11.0	3231	8	US-08-754-311B-1	Sequence 1, Appl1
28	87.5	11.0	10278	13	US-09-820-788-3	Sequence 20319, A
29	87.5	11.0	10278	13	US-10-094-749-1507	Sequence 1507, App
30	87	10.9	2200	13	US-10-369-493-45445	Sequence 45445, A
31	86.5	10.9	1587	12	US-10-205-219-182	Sequence 182, App
32	86	10.8	1963	13	US-10-205-219-182	Sequence 97742, A
33	86	10.8	2179	13	US-10-027-632-97742	Sequence 97742, A
34	86	10.8	2179	14	US-10-027-632-97742	Sequence 31940, A
35	85.5	10.7	1960	12	US-10-369-493-31940	Sequence 502, App
36	85.5	10.7	2208	13	US-10-117-722-502	Sequence 502, App
37	85.5	10.7	2208	15	US-10-037-270-502	Sequence 20383, A
38	85	10.7	1055	13	US-10-029-386-20383	Sequence 3834, App
39	85	10.7	1383	15	US-10-156-761-3834	Sequence 788, App
40	85	10.7	1793	10	US-09-887-576-788	Sequence 226, App
41	85	10.7	6930	14	US-10-098-844-226	Sequence 1, Appl1
42	85	10.7	53522	11	US-09-904-968A-1	Sequence 452, App
43	85	10.7	9025608	15	US-10-156-761-1	Sequence 452, App
44	84.5	10.6	969	13	US-10-244-830-452	Sequence 452, App
45	84.5	10.6	969	13	US-10-195-835-452	Sequence 452, App

ALIGNMENTS

RESULT 1
US-09-809-545A-1
Sequence 1, Application US/09809545A
Patent No. US2002010804A1
GENERAL INFORMATION:
APPLICANT: Stanton, Lawrence W.
TITLE OF INVENTION: SECRETED FACTORS
FILE REFERENCE: SCIOS.017A
CURRENT APPLICATION NUMBER: US/09/809,545A
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1340
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-809-545A-1

Alignment Scores:
Pred. No.: 6,97e-86
Score: 796.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Length: 1340
Matches: 148
Conservative: 0
Mismatches: 0

Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

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DB 535 ATGACTATATAAAGCCGCTGACCCCTACACCAATGGCTGGAAATTAATCCAGTTGTG 594
QY 21 G1yAlaVala1TyrSerProAspPheTyrAlaGlyThrValleuCyseGlnAlaAsnGln 40
DB 595 GGGCCGGCTTACACCCCGGACTTCTATGACAGCAGCGGTGCTGTCGACGAGCCAGC 654
QY 41 GluGlySerSerMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
DB 655 GAGGAGCTTCCATGCTACAGTGGCCGACGTTCACTTGTATTAATCTTCCAGTCCCTGGC 714
QY 61 PheProTyrProAlaAlaThrAlaAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 80
DB 715 TTTCATATCCGGCGCCGACCTGTCAGCTGCATACGAGGGGCTCACCTTCGAGGCGCT 774
QY 81 GlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProProProleProAlaTyr 100
DB 775 GGTGCACCGGTGACCAACCTTCAGAGCTGGCGCCGCCCAATCCCGGCTAT 834
QY 101 G1yGlyValaValaTyrGlnGluProValTyrGlyAsnLysLeuGlnGlyGlyTyrAla 120
DB 835 GGGGAGTAGTGTATCAAGAGCCAGTGTATGGCAATTAATGCTACAGGGGTATAGCT 894
QY 121 AlaTyrArgTyrAlaGlnProThrProAlaThrAlaAlaAlaTyrSerAspSerTyrGly 140
DB 895 GCATACCGCTACGGCCGACCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 954
QY 141 ArgValaTyrAlaAlaAspProTyr 148
DB 955 CGAGTTATGCTGCGCAGCCCTAC 978
```

RESULT 2

US-09-794-591-1
Sequence 1, Application US/09794591
Patent No. US20010018198A1
GENERAL INFORMATION:
APPLICANT: Pulet, Stefan M.
APPLICANT: Shibata, Hiroki
TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins.
FILE REFERENCE: CE 3093
CURRENT APPLICATION NUMBER: US/09/794,591
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/145,391
PRIOR FILING DATE: 1998-09-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2372
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (987) .. (1979)
US-09-794-591-1

Alignment Scores:
Pred. No.: 6,31e-71 Length: 2372
Score: 674.00 Matches: 136
Percent Similarity: 83.23% Conservative: 3
Best Local Similarity: 81.44% Mismatches: 8
Query Match: 84.67% Indels: 21
DB: 9 Gaps: 2

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-794-591-1 (1-2372)

QY 1 MetThraenlyblysaValaValaAspProTyrThrAnslYTrpLysLeuAsnProValVal 20

```
DB 1572 ATGACAAATATAAAGACCGTCAACCTTATACAAATGGCTGGAAATGATTCAGTTGTG 1631
QY 21 G1yAlaVala1TyrSerProAspPheTyrAlaGlyThrValleuCyseGlnAlaAsnGln 40
DB 1632 GGTGCAGTCTTACAGTCCCAATTTCTATGACGACGCTCTGTGTCGACGACACAG 1691
QY 41 GluGlySerSerMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
DB 1692 GAGGAGCTTCCATGATACAGTGCCCGAGTTCACTTGTATTAATCTTCCAGTCCAGGC 1751
QY 61 PheProTyrProAlaAlaThrAlaAlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArg 80
DB 1752 TTCCCTATCCAGACACACCGCGCGGCTTACCGAGGGGCGACCTGCAAGCGCGC 1811
QY 81 GlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProProProleProAlaTyr 100
DB 1812 GGTGCACCGGTGACCAACCTTCAGGGCGCGCCGCCGCCGATCCCGGCTAC 1871
QY 101 G1yGlyValaValaTyr-GlnGluProValTyrGlyAsnLysLeuGlnGlyGlyTyrAla 120
DB 1872 GGGGAGTGTGTTATCCAGAGATGATTTATGCTGACAGC---ATTATGCTGTTATGC 1928
QY 120 AlaTyrArgTyrAlaGlnProThrProAlaThrAlaAlaAlaTyrSerAspSer----- 138
DB 1929 TGCATACCGCTACGCCAGCTACCCCTGCACTGCGCTGCTTACAGTACAG-AAATC 1987
QY 139 -----TyrGlyArgVa 142
DB 1988 AGTTCGCTTCTTGCAGCAGATGAATTTCTTGTACACCTCTGCAGTTACGAGAGGT 2047
QY 142 T1yAlaAlaAspProTyr 148
DB 2048 TTATGCTGCGCAGCCCTAC 2066
```

RESULT 3

US-09-919-039-266
Sequence 266, Application US/09919039
Publication No. US2003010887A1
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 266
LENGTH: 1843
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US2003010887A1 253783.3
NAME/KEY: unsure
LOCATION: 1824
OTHER INFORMATION: a, t, c, g, or other
US-09-919-039-266

Alignment Scores:
Pred. No.: 3,78e-43 Length: 1843
Score: 441.50 Matches: 96
Percent Similarity: 51.02% Conservative: 4
Best Local Similarity: 48.98% Mismatches: 19
Query Match: 55.46% Indels: 77
DB: 11 Gaps: 5

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-919-039-266 (1-1843)

QY 1 MetThraenlyblysaValaValaAspProTyrThrAnslYTrpLysLeuAsnProValVal 20


```
DB 1228 ATGACCAAGAAAGGAGGAGGAAACCCCTACACCAACGGCTGAAGCTAAATCCAGGAGTC 1287
QY 21 GYALVALTYRSEPRAPSPHETRYALAGLYTH-ValLeuLeuCySGlnAlaAngln 40
DB 1288 GGGCGAGCTTACGGGCGCTGAAATCTATGACGTAGC----- 1323
QY 41 GlnGlySerSerMetYrSerGlyProSerSerLeuValYrThrSerAlaMetProGly 60
DB 1324 -----GGG 1326
QY 61 PheProTYrProAlaAlaThrAlaAlaAlaAlaTYrArgGlyAlaHisLeuArgGlyArg 80
DB 1327 TTCCTTACCCCAACCCGACACCGGACAGCGCTTGCCTTACCGGGGCGCACATCTTCGGGGCCGG 1386
QY 81 GYARThrValTYrAsnThrPheArgAlaAlaAlaProProProProLeuProAlaTYr 100
DB 1387 GGGCGGGGCGGTATATATACATTTCCGGCTGCGCCACCCCGCCATCCGACTTAC 1446
QY 101 GYGLY----- 102
DB 1447 GGAGCGGCACTGAGACAAAGCTTTGTTAAATGCAATGCCATGGGGGGGCTGGCACCG 1506
QY 102 ----- 102
DB 1507 TGCCCTCCCTCCTCTCAGACAGACCGAGCGGCTTACCCCACTCTCCAGCGTTCCCA 1566
QY 103 -----ValValTYrGlnGlnProValTYrGlyAsnLys 113
DB 1567 CCACCTTCTTGTCGGTTGCTTCCAGAGGTGTGTATCAGATGATTTATGTGTGCTGAG 1626
QY 114 LeuLeuGlnGlyGlyTYrAlaAlaTYrArgTYrAlaGlnProThrProAlaThrAlaAla 133
DB 1627 ---ATTATAGAGGCTTACGAGCCTTACAGTACGCTTACGCCCT---GAGAGGGGGCA 1680
QY 134 AlaTYrSerAspSerTYrGlyArgValTYr---AlaAlaAspProTYr 148
DB 1681 GCTTACAGGCAAGTATACGAGAGTCTACGAGCTGCCAGCCCGTAC 1728

RESULT 4
US-10-094-749-287
; Sequence 287, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 287
```

```
; LENGTH: 1558
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-094-749-287
Alignment Scores:
Pred. No.: 6,42e-42 Length: 1558
Score: 430.50 Matches: 98
Percent Similarity: 63.69% Conservative: 9
Best Local Similarity: 58.33% Mismatches: 37
Query Match: 54.08% Indels: 25
DB: 13 Gaps: 6

US-09-809-545a-2_copy_1_148 (1-148) x US-10-094-749-287 (1-1558)
QY 1 MCTTRAsnLysLysAlaValAsnProTYrThrAsnGlyTyrLysLeuAsnProValVal 20
DB 854 ATGACCAATAGAAAGATGATGCTACACCATATGCAAAATGTTGAAATTAAGCCAGTAGTT 913
QY 21 GYALVALTYRSEPRAPSPHETRYALA----- 30
DB 914 GGAGCTGTATATGTCGGAGATTATATGACGATTCACTTCAAGACAGATGTCCTTA 973
QY 31 GYlThr-ValLeuLeuCySGlnAlaAnglnGlnGlySerSerMetYrSerGlyProSe 50
DB 974 GCCAATGATGACAGAGTGCCTTATCAGGAGAGGGGGTATCAACACTTACATT--CCT-- 1030
QY 50 rSerLeuValTYrThrSerAlaMetProGlyPheProTYrPro---AlaAlaThrAlaAl 69
DB 1031 ---TTAATCATCTTCCCTTATGTTCTGCTTCCCTTACCTTACGACGCAACGCGC 1086
QY 69 aAlaAlaTYrArgGlyAlaAlaHisLeuArgGlyArgTYrAsnThrPheAr 89
DB 1087 AGCCGCTTCAAGAGAGCCCATTTGAGGGGCGAGGGCGGACAGTATATGTCGAGTCGG 1146
QY 89 gAlaAlaLapProProProProLeuProAlaTYrGlyValValTYrGlnGlnProVa 109
DB 1147 A---GGGTAACCTCCNAACAGCATCCCGCTATCCAGGTGTGTATACGAGACGAGTT 1203
QY 109 lTYrGlyAsnLysLeuLeuGlnGlyTYrAlaAlaTYrArgTYrAlaGlnProThrPr 129
DB 1204 TTACGCTGTCTGAC---CTTATGTGATATGACGCTTACAAATATGACACCCGCTAC 1260
QY 129 oAlaTYr-----AlaAlaAlaTYrSerAspSerTYrGlyAr 141
DB 1261 TGCACCGGACGACCGCTGCTGACCGCGCTGACGCGCTTACGAGTATATGCGAG 1320
QY 141 gValTYrAlaAlaAspProTYr 148
DB 1321 GGTGTACACAGCGCACCCCTTAC 1342

RESULT 5
US-10-359-385-5
; Sequence 5, Application US/10359385
; Publication No. US20030143622A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Aina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/10/359,385
; PRIOR FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/176,657
; PRIOR FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
```

ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 1250374
US-10-359-385-5

Alignment Scores:

Pred. No.: 9.38e-36 Length: 1506
Score: 379.00 Matches: 86
Percent Similarity: 59.63% Conservative: 10
Best Local Similarity: 53.42% Mismatches: 37
Query Match: 47.61% Indels: 29
DB: 13 Gaps: 6

US-09-809-545a-2_copy_1_148 (1-148) x US-10-359-385-5 (1-1506)

QY 1 MetThrAnlyYsAlaValAsnProTyrThrAnlyTTrpYsLeuAsnProValVal 20
DB 768 ATGACCAATAGAGAGATGTCACACCATATGCAATATGTTGAAATTAAGCCGATGTT 827
QY 21 G1ValAlaValTyrSerProAspPheTyrAlaGlyThrValLeuLeuCyGlnAlaAsn--- 39
DB 828 GGAAGCTATATATGTCGAGCTTATATGCAATTCACAGCTTTCACAGAGATGTCTCTTA 887
QY 40 ---GlnGlySerSerMetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
DB 888 GGCAATGATGACAGATGCCCCCTATCAGAAAGGGGATATCAACACTTACATTCCTTTA 947
QY 57 AlaMetProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaTyrArgGlyAla 75
DB 948 ATCTCTCTGCTCTTCCCTTACCTTACCTGACGACGACGAGCGCTTTCAGAGAGCC 1007
QY 76 HistLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaProProPro 95
DB 1008 CATTGAGGGGACAGGGGCGACATATATGTCAGTCCGA---GGCGTACCTCCACAA 1064
QY 96 ProLeuProAlaTyrGlyValValTyrGlnGluProValTyrGlyAsnYsLeuLeu 115
DB 1065 GCCATCCCCGCTATCC----- 1081
QY 116 GlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
DB 1082 AGGGGTGATATGACGCTTACAGATATGCAACAGCTCTACTGACCGCAGCCAGCCGCT 1141
QY 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
DB 1142 GCTCAGCGCTGACGCGCTTACAGTATGACGCTTATGCAAGGAGTACACAGCCGACCC 1201
QY 148 Tyr 148
DB 1202 TAC 1204

RESULT 6

US-10-104-047-659
Sequence 659, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20030236392A1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10104_047
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 659
LENGTH: 2397
TYPE: DNA
ORGANISM: Homo sapiens
US-10-104-047-659

Alignment Scores:

Pred. No.: 3.62e-07 Length: 2397

Score: 143.00 Matches: 30
Percent Similarity: 68.89% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 6
Query Match: 17.96% Indels: 8
DB: 12 Gaps: 1

US-09-809-545a-2_copy_1_148 (1-148) x US-10-104-047-659 (1-2397)

QY 112 AsnYsLeuLeuGlnGlnGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
DB 2058 TCTTCTCTCTCTGATAGGATGATATGACGCTTACAGATATGCAACAGCTGCTACTGCAAC 2117
QY 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyr 143
DB 2118 GCAGCAGCCGCTGCTGACGCGCTTACAGTACGCTTATGCAAGGATGTATC 2177
QY 144 AlaAlaAspProTyr 148
DB 2178 ACAGCCGACCCCTAC 2192

RESULT 7

US-09-974-300-1655
Sequence 1655, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
FILE REFERENCE: Expression
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1655
LENGTH: 657
TYPE: DNA
ORGANISM: Bacillus licheniformis
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(657)
OTHER INFORMATION: n = A,T,C or G
US-09-974-300-1655

Alignment Scores:

Pred. No.: 0.055 Length: 657
Score: 94.00 Matches: 38
Percent Similarity: 40.15% Conservative: 17
Best Local Similarity: 27.74% Mismatches: 58
Query Match: 11.81% Indels: 24
DB: 10 Gaps: 8

US-09-809-545a-2_copy_1_148 (1-148) x US-09-974-300-1655 (1-657)

QY 2 ThrAsnYsLeuValAsnProTyrThrAnlyTTrpYsLeuAsnProValValGly 21
DB 100 ACAAAAAAAAAAACCAATTAAACA---ACCAAGGGCTTAAACGAAACGAGTAACTCC 156
QY 22 -----AlaValTyrSerProAspPhe---TyrAlaGlyThrValLeuLeu 35
DB 157 TTAACGCCCCCCCCGGGCTTTTTCACAGATTTCTTATACAAAACCTGGGCTTCTT 216
QY 36 CyGlnAlaAsnGlnGlySerSerMetTyrSerGlyProSerSerLeuValTyrThr 55
DB 217 ACCACCAAAAAAAAAACAGAGTCCGGTTTC-----CCCTTAAGGAAAAATTAAAC 267
QY 56 SerAlaMetProGlyPheProTyrProAlaAlaThrAlaAlaAlaTyrArgGlyAla 75
DB 268 CCTTTAAACCAATTCACTTTTAACTTTAAACGCAACCCCAATCCCAACCCCTC 327

QY 76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProPro 95
|||:::|||||
Db 328 CAAATTTTCATCTCTGGT-----TTCAAAATTTTTCATCATTAACCCCGG 378
QY 96 ProIleProAla-----TyrGlyGlyValValTyrGlnGlu 107
|||:::|||||
Db 379 AAAAACCCCTCCCGGTACAACTTATTTTTCAAATACACGGGCTTGGCTCGGGA 438
QY 108 ProValTyrGlyAsnTyrLeuLeuGlnGlyGly-----TyrAlaAlaTyr 122
|||:::|||||
Db 439 CCAATTAACCCCAAC---CTGGCCAAAGGCGCCAGGTTTATCTCCCTTAC 486

RESULT 8
US-10-027-632-24830
; Sequence 24830, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24830
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24830

Alignment Scores:
Pred. No.: 0.0899 Length: 699
Score: 92.50 Matches: 41
Percent Similarity: 37.76% Conservative: 13
Best Local Similarity: 28.67% Mismatches: 41
Query Match: 11.62% Indels: 48
DB: 13 Gaps: 6

US-09-809-545a-2_copy_1_148 (1-148) x US-10-027-632-24830 (1-699)

QY 25 SerProAspPheTyrAlaGlyThrValLeuLeuCysGlnAla-AasnGlnGlySerse 44
:::|||||
Db 84 ACACCAAGACAGAAAGGGGTCTCAATCCCTCTGTGCTCTGCTTCA-----YCTGG 134
QY 44 rMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyr-- 63
|||:::|||||
Db 135 ACAAGTCTCAGGCCCAAGCATCTC---CAGGWAAGACCAAGGGCTGCTGCTTACCA 191
QY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyrArgG 74
|||:::|||||
Db 192 CTGACCTCAACAAGTCCCTCCCAAGTGCAGGCTCCACCTCTCTCCCTTGCAGAG 251
QY 74 yAlaHisLeuArgGlyArg-----80
|||:::|||||
Db 252 AGAARACCTAAATCGAAATCTCAACGTGATAGAGGTACAGAGTCTTGGCTCTCC 311
QY 81 -----GlyArgThrValTyrAsnThrPheArgAlaAlaAlaProProPro 95

Db 312 TGTGCCCCCTGACCCGGGACACCTCTCCACGACCATGTCTGAGATCTCCCTCTCC 371
QY 95 oProIleProAlaTyrGlyGlyVal-----Val-TyrGlnGluProValTyrGlyA 112
|||:::|||||
Db 372 TCAGGCCCTTCTCTAGTGGGGTCTCTGGAATGCTCTTCCCAACCATCTACGCA 431
QY 112 snLys-LeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
|||:::|||||
Db 432 ATCCGCTCTTCCAGGC-----CCGAGTCCAGGCCCG 464
QY 132 Ala 132
|||
Db 465 GCA 467

RESULT 9
US-10-027-632-24831
; Sequence 24831, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24831
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24831

Alignment Scores:
Pred. No.: 0.0899 Length: 699
Score: 92.50 Matches: 41
Percent Similarity: 37.76% Conservative: 13
Best Local Similarity: 28.67% Mismatches: 41
Query Match: 11.62% Indels: 48
DB: 13 Gaps: 6

US-09-809-545a-2_copy_1_148 (1-148) x US-10-027-632-24831 (1-699)

QY 25 SerProAspPheTyrAlaGlyThrValLeuLeuCysGlnAla-AasnGlnGlySerse 44
:::|||||
Db 84 ACACCAAGACAGAAAGGGGTCTCAATCCCTCTGTGCTCTGCTTCA-----YCTGG 134
QY 44 rMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyr-- 63
|||:::|||||
Db 135 ACAAGTCTCAGGCCCAAGCATCTC---CAGGWAAGACCAAGGGCTGCTGCTTACCA 191
QY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyrArgG 74
|||:::|||||
Db 192 CTGACCTCAACAAGTCCCTCCCAAGTGCAGGCTCCACCTCTCTCCCTTGCAGAG 251
QY 74 yAlaHisLeuArgGlyArg-----80
|||:::|||||
Db 252 AGAARACCTAAATCGAAATCTCAACGTGATAGAGGTACAGAGTCTTGGCTCTCC 311

```
OY 81 -----GlyArgThrValTyrAsnThrPheArgAlaAlaLarProPro 95
DB 312 TGGTCCCCCTGACCCGGGACACCTCTCCACGACCATGTGAGATGTCCTCTCC 371
OY 95 oProIleProAlaTyrGlyVal-----Val-TyrGlnGluProValTyrGlyA 112
DB 372 TCCAGGCCCTTCTTACAGTGGGGTCTCTGGAATGCTCTTCCCAAAACCATCTACGCA 431
OY 112 snLys-LeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
DB 432 ATCTGCTCTTCCGAGGC-----CCCACTCCAGCCCGC 464
OY 132 Ala 132
DB 465 GCA 467

RESULT 10
US-10-027-632-24832
; Sequence 24832, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24832
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24832

Alignment Scores:
Pred. No.: 0.0899 Length: 699
Score: 92.50 Matches: 41
Percent Similarity: 37.76% Conservative: 13
Best Local Similarity: 28.67% Mismatches: 41
Query Match: 11.62% Indels: 48
DB: 13 Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-027-632-24832 (1-699)
OY 25 SerProAspPheTyrAlaGlyThrValLeuLeuGlnAla-AbsGlnGluGlySerse 44
DB 84 ACACCAACAGAGAGGGGTCTCATCTCTGCTGCTGCTTCA-----YCTGG 134
OY 44 tMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyr-- 63
DB 135 ACAAGTCTCAGGCCGACCATCTC---CAGGWAAGCCAGGCGCTGCTCTTACCA 191
OY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyrArgG 74
DB 192 CTGACCTCACAAGTCTCTCCCAAGTGCAGCTCCACCTCTCTCTGCCCCAAGG 251
OY 74 yAlaHleuValGlyArg----- 80
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DB 252 AGAARACCTAAATCGAAATCTCCAGTGTAGAGGTACAGACTCTTGCCCTCTCC 311
OY 81 -----GlyArgThrValTyrAsnThrPheArgAlaAlaLarProPro 95
DB 312 TGGTCCCCCTGACCCGGGACACCTCTCCACGACCATGTGAGATGTCCTCTCC 371
OY 95 oProIleProAlaTyrGlyVal-----Val-TyrGlnGluProValTyrGlyA 112
DB 372 TCCAGGCCCTTCTTACAGTGGGGTCTCTGGAATGCTCTTCCCAAAACCATCTACGCA 431
OY 112 snLys-LeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
DB 432 ATCTGCTCTTCCGAGGC-----CCCACTCCAGCCCGC 464
OY 132 Ala 132
DB 465 GCA 467

RESULT 11
US-10-027-632-24830
; Sequence 24830, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24830
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24830

Alignment Scores:
Pred. No.: 0.0899 Length: 699
Score: 92.50 Matches: 41
Percent Similarity: 37.76% Conservative: 13
Best Local Similarity: 28.67% Mismatches: 41
Query Match: 11.62% Indels: 48
DB: 14 Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-10-027-632-24830 (1-699)
OY 25 SerProAspPheTyrAlaGlyThrValLeuLeuGlnAla-AbsGlnGluGlySerse 44
DB 84 ACACCAACAGAGAGGGGTCTCATCTCTGCTGCTGCTTCA-----YCTGG 134
OY 44 tMetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyr-- 63
DB 135 ACAAGTCTCAGGCCGACCATCTC---CAGGWAAGCCAGGCGCTGCTCTTACCA 191
OY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyrArgG 74
DB 192 CTGACCTCACAAGTCTCTCCCAAGTGCAGCTCCACCTCTCTCTGCCCCAAGG 251
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QY 74 yAlaHisLeuArgGlyArg----- 80
Db 252 AGAARACCTAAATCGAATCTCCAGCTGATAGAGGTACAGAGCTTGGCTTCC 311
QY 81 -----GlyArgThrValTyrAsnThrPheArgAlaAlaIleProPro 95
Db 312 TGTGCCCCCTGACCCGGGACACCTCTCCACAGCATGTGAGATGTCCTCTCC 371
QY 95 oProIleProAlaTyrGlyVal-----Val-TyrGlnGluProValTyrGly 112
Db 372 TCCAGGCCCTTCTTACAGTGGGCTCTCTGGAATGCTCTTCCAAACCATCTACGCA 431
QY 112 snlys-LeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
Db 432 ATCTGCTCTTCCGAGC-----CCGAGTCCAGCCCC 464
QY 132 Ala 132
Db 465 GCA 467
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RESULT 12

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US-10-027-632-24831
; Sequence 24831, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24831
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24831
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Alignment Scores:

Pred. No.:	0.0899	Length:	699
Score:	92.50	Matches:	41
Percent Similarity:	37.76%	Conservative:	13
Best Local Similarity:	28.67%	Mismatches:	41
Query Match:	11.62%	Indels:	48
DB:	14	Gaps:	6

US-09-809-545A-2_COPY_1_148 (1-148) x US-10-027-632-24831 (1-699)

```
QY 25 SerProAspPheTyrAlaGlyThrValLeuLeuCysGlnAla-AsnGlnGluGlySerse 44
Db 84 ACACCGACAGAAACGGGGTCTCAATCCCTGCTGCTGCGTCA-----YCTGG 134
QY 44 rMetTySerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyr-- 63
Db 135 ACAAGTCTCAGGCCCGCCAGCATCTC---CAGGAGACCCAGGGGCTGCTGCTTACCA 191
QY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyrArgGly 74
Db 192 CTGACCTCACCAGTCTCCTCCCAAGTGCAGGCTTCACCTCTCTGCTTGGCCAGAGG 251
```

```
QY 74 yAlaHisLeuArgGlyArg----- 80
Db 252 AGAARACCTAAATCGAATCTCCAGCTGATAGAGGTACAGAGCTTGGCTTCC 311
QY 81 -----GlyArgThrValTyrAsnThrPheArgAlaAlaIleProPro 95
Db 312 TGTGCCCCCTGACCCGGGACACCTCTCCACAGCATGTGAGATGTCCTCTCC 371
QY 95 oProIleProAlaTyrGlyVal-----Val-TyrGlnGluProValTyrGly 112
Db 372 TCCAGGCCCTTCTTACAGTGGGCTCTCTGGAATGCTCTTCCAAACCATCTACGCA 431
QY 112 snlys-LeuLeuGlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
Db 432 ATCTGCTCTTCCGAGC-----CCGAGTCCAGCCCC 464
QY 132 Ala 132
Db 465 GCA 467
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RESULT 13

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US-10-027-632-24832
; Sequence 24832, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24832
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-24832
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Alignment Scores:

Pred. No.:	0.0899	Length:	699
Score:	92.50	Matches:	41
Percent Similarity:	37.76%	Conservative:	13
Best Local Similarity:	28.67%	Mismatches:	41
Query Match:	11.62%	Indels:	48
DB:	14	Gaps:	6

US-09-809-545A-2_COPY_1_148 (1-148) x US-10-027-632-24832 (1-699)

```
QY 25 SerProAspPheTyrAlaGlyThrValLeuLeuCysGlnAla-AsnGlnGluGlySerse 44
Db 84 ACACCGACAGAAACGGGGTCTCAATCCCTGCTGCTGCGTCA-----YCTGG 134
QY 44 rMetTySerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyr-- 63
Db 135 ACAAGTCTCAGGCCCGCCAGCATCTC---CAGGAGACCCAGGGGCTGCTGCTTACCA 191
QY 64 -----ProAlaAlaThrAlaAlaAlaAlaTyrArgGly 74
Db 192 CTGACCTCACCAGTCTCCTCCCAAGTGCAGGCTTCACCTCTCTGCTTGGCCAGAGG 251
```

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Db 192 CTGACCTCACCAGTCCCTCCCAAGTGCAGCAGCTCCACCTCTCTCCCTTGCCAGAG 251
Oy 74 yAlaHleuArglyArg----- 80
Db 252 AGAARACCTTAAATCGAAATCTCCACGTGATAGAGTACAGATCTTGCCCTTCC 311
Oy 81 -----GlyArgThrValTyrAsnThrPheArgAlaAlaProProP 95
Db 312 TGGGCCCCCTGACCGGGGACACCTCTCCACAGACATGTCTGATGTCCCTCTCC 371
Oy 95 oProlleProAlaTyrlylyVal-----Val-TyrGlnGluProValTyrly 112
Db 372 TCCAGCCCTCTTCTTACAGTGGGCTCTCGAATGTCTTCCCAACCATCTACCCAA 431
Oy 112 enlyG-leuLeuGlnGlylyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr 131
Db 432 ATCCTGCTCTTCCAGGC-----CCAGTCCAGCCCG 464
Oy 132 Ala 132
Db 465 GCA 467

RESULT 14
US-10-301-822-25
; Sequence 25, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, AND
; FILE REFERENCE: MEM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(9192)
US-10-301-822-25

Alignment Scores:
Pred. No.: 2.95 Length: 11447
Score: 92.50 Matches: 28
Percent Similarity: 39.22% Conservative: 12
Best Local Similarity: 27.45% Mismatches: 41
Query Match: 11.62% Indels: 21
DB: 13 Gaps: 4

US-09-809-545A-2_COPY_1_148 (1-148) x US-10-301-822-25 (1-11447)
Oy 50 SerSerleuValTyrThrSerAlaMetProGlyPheProTyrProAlaAlaThrAlaAla 69
Db 6332 AACCATGTAAATATGCGAGCCCTGCACACTGACTCAATAT---AAAATTACTGTATT 6288
Oy 70 AlaAlaTyrArg-----GlyAlaHisleuArglyArgGlyArgThrVal----- 84
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Db 6289 GCTGTATTAGAGATGAGATGAGTGGCCATCTAACAGAAATGGAAGAACTGGGAGACTC 6348
Oy 85 -----TyrAsnThrPheArgAlaAla 92
Db 6349 CTTCCTCTCAGAACATACATCTCTGACGAATGGTATACAGATTCAGGGTCTCTG 6408
Oy 93 ProProProProlleProAlaTyrlylyValValTyrGlnGluProValTyrlyAsn 112
Db 6409 GATCCTTCAACCTCTCTCAGTCTTGATATTAATAATGATATATAGCCAGTGGGTTCCAAT 6468
Oy 113 LysLeuLeuGln-----GlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrPro 129
Db 6469 GAGCCCATGGAACCTTTGTTGGAGAAATGACATCATATACCTTACACAACTTCATCC 6528
Oy 130 AlaThr 131
Db 6529 AGCACC 6534

RESULT 15
US-10-177-293-60
; Sequence 60, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatz, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Ganavarrpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegül
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 11447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-177-293-60

Alignment Scores:
Pred. No.: 2.95 Length: 11447
Score: 92.50 Matches: 28
Percent Similarity: 39.22% Conservative: 12
Best Local Similarity: 27.45% Mismatches: 41
Query Match: 11.62% Indels: 21
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DB: 15 Gaps: 4
US-09-809-545a-2_copy_1_148 (1-148) x US-10-177-293-60 (1-11447)
QY 50 SerSerLeuValTyrThrSerIleMetProGlyPheProTyrProAlaIleThrAlaIle 69
   ::::::::::::::::::::|||
Db 6232 AACAAATGTAATCTGCAGCCCTGCACCTGCACATCCATAT--AAATTAAGTTATT 6288
   |||
QY 70 AlaAlaTyrArg-----GlyAlaHisLeuArgGlyArgGlyVal----- 84
   |||
Db 6289 GCTGTTATGAGATGAGATGAGTGGCCATCTAACAGAAATGAGAAAGAACTGTGGGACTC 6348
   |||
QY 85 -----TyrAsnThrPheArgAlaAla 92
   |||
Db 6349 CTTCTCTCTCAGAACATACATCTCTGACGAATGGTATACAAAGATTCAAGGTCTCTGG 6408
   |||
QY 93 ProProProProIleProAlaTyrGlyGlyValValTyrGlnIleProValTyrGlyAsn 112
   |||
Db 6409 GATCTCTCACTTCTCCAGTTCTTGATATAAATAGTATATAAGCCAGTGGGTTCCAAAT 6468
   |||
QY 113 LysLeuLeuGln-----GlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrPro 129
   ::::::::::::::::::::|||
Db 6469 GAGCCCATGGAAGCCTTGTGTGGAGAAATGACATCATATACCTTACACAATCTCAATCCC 6528
   |||
QY 130 AlaThr 131
   ::::::::::
Db 6529 AGCACC 6534
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Search completed: January 15, 2004, 11:19:58
Job time : 207.852 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: January 15, 2004, 08:41:56 ; Search time 48,9117 Seconds
(without alignments)
1335.564 Million cell updates/sec

Title: US-09-809-545a-2_COPY_1_148

Perfect score: 796

Sequence: 1 MTNRKAVNPYINGMKLNPV.....PATNAASPSYGRVYADPY 148

Scoring table: BLOSUM62
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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=Issued_Patents_NA -QFWT=fasted -SUFFIX=nt1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEOBJECT -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-BEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- Issued Patents NA:*
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 - 2: /cg2_6/prodata/2/ina/5B_COMB.seq:*
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 - 4: /cg2_6/prodata/2/ina/5B_COMB.seq:*
 - 5: /cg2_6/prodata/2/ina/5A_COMB.seq:*
 - 6: /cg2_6/prodata/2/ina/5B_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	674	84.7	2372	3	US-09-145-391-1
2	379	47.6	1506	4	US-09-176-657-5
3	379	47.6	1506	4	US-09-421-299-5
4	93	11.7	914	2	US-08-935-450-10
5	92.5	11.6	28958	1	US-08-258-261B-6
6	92.5	11.6	28958	1	US-08-456-837-6
7	92.5	11.6	28958	1	US-08-457-342-6
8	92.5	11.6	28958	1	US-08-457-646A-6
9	92.5	11.6	28958	1	US-08-458-076A-6
10	92.5	11.6	28958	1	US-08-764-233A-4
11	92.5	11.6	28958	1	US-08-457-335A-6
12	92.5	11.6	28958	1	US-08-729-214-6

13	92.5	11.6	28958	3	US-09-028-934-6	Sequence 6, Appli
14	92.5	11.6	49377	1	US-08-764-233A-1	Sequence 1, Appli
15	91	11.4	821	3	US-08-990-823-62	Sequence 62, Appli
16	91	11.4	821	4	US-09-477-135A-62	Sequence 62, Appli
17	91	11.4	1896	4	US-09-343-011B-4	Sequence 4, Appli
18	89.5	11.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
19	89.5	11.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
20	87.5	11.0	3231	1	US-08-195-153-1	Sequence 1, Appli
c 21	86.5	10.9	4403765	3	US-09-103-840A-2	Sequence 1, Appli
c 22	86.5	10.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
23	85.5	10.7	1140	3	US-09-023-1173-4	Sequence 4, Appli
24	85.5	10.7	2208	4	US-09-620-312D-502	Sequence 502, App
25	85	10.7	53526	3	US-08-658-136-2	Sequence 2, Appli
26	85	10.7	53577	3	US-08-658-136-1	Sequence 1, Appli
27	84.5	10.6	1462	1	US-08-552-142A-16	Sequence 16, Appli
28	84.5	10.6	1494	4	US-09-255-502-1	Sequence 1, Appli
29	84.5	10.6	1496	6	RE34606-1	Patent No. RE34,60
30	84.5	10.6	1497	1	US-08-322-677A-6	Sequence 6, Appli
31	84.5	10.6	1497	1	US-08-322-676-6	Sequence 6, Appli
32	84.5	10.6	1497	3	US-08-898-218-6	Sequence 6, Appli
33	84.5	10.6	1497	3	US-08-848-793-6	Sequence 6, Appli
34	84.5	10.6	1497	4	US-09-445-270-1	Sequence 1, Appli
35	84.5	10.6	1497	4	US-09-178-173A-1	Sequence 1, Appli
36	84.5	10.6	1497	4	US-08-322-678-6	Sequence 6, Appli
37	84.5	10.6	1497	6	5472855-1	Patent No. 5472855
38	84.5	10.6	1513	4	US-09-178-155-1	Sequence 1, Appli
39	84.5	10.6	1868	1	US-08-069-863-1	Sequence 1, Appli
40	84.5	10.6	1868	1	US-08-309-069-1	Sequence 1, Appli
41	84.5	10.6	1868	1	US-08-562-833-1	Sequence 1, Appli
42	84.5	10.6	1868	4	US-09-659-749-1	Sequence 1, Appli
43	84.5	10.6	1868	4	US-09-672-105-1	Sequence 1, Appli
44	84.5	10.6	1868	5	PCR-US95-05520-1	Sequence 1, Appli
45	83.5	10.5	1352	1	US-08-552-142A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-145-391-1
; Sequence 1, Application US/09145391
; Patent No. 6194171
; GENERAL INFORMATION:
; APPLICANT: Polster, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Atrialin-2 Binding Proteins.
; FILE REFERENCE: CB 3093
; CURRENT APPLICATION NUMBER: US/09/145,391
; CURRENT FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (987)..(1979)
US-09-145-391-1

Alignment Scores:
Pred. No.: 4,26e-59
Score: 674.00
Percent Similarity: 83.23%
Best Local Similarity: 81.44%
Query Match: 84.67%
DB: 3
Gaps: 2

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-145-391-1 (1-2372)

Qy 1 MetThrAsnLysValAlaValAsnProTyrThrAsnGlyTTPLeuAsnProValVal 20
Db 1572 ATGACAAATTAAGACCGCTCAACCTTATACAAATGCTGGAATTCACCTGTC 1631

QY 21 G1YAlaValTyrSerProaepheTyrAlaGlyThrValLeuLeuCySGlnAlaAsnGln 40
Db 1632 GGGAGCTCTACAGCTCCGAAATCTATGACAGCGAGCTGTTGGCCAGCCACAG 1691
QY 41 GluGlySerSermetTyrSerGlyProSerSerLeuValTyrThrSerAlaMetProGly 60
Db 1692 GAGGAGCTTCATGATGACAGTGGCCCGAGTTCACTTATATCTTCTGCAATGCCAGGC 1751
QY 61 PheProTyrProAlaAlaThrAlaAlaAlaTyrArgGlyAlaHisLeuAlaArgGlyArg 80
Db 1752 TTCCTCGATACAGACGACCGCCGCGCCCTACCGAGGGGCGACCTGCCAGCGCCGC 1811
QY 81 G1YArgThrValTyrAsnThrPheArgAlaAlaAlaProProProPheProAlaTyr 100
Db 1812 GGTGCGACCGGTGACCAACCTTCAGGGCGGCGGCGCCCGCCCGCCAGTCCGCGCTAC 1871
QY 101 G1YGlyValValTyrGlnGluProValTyrGlyAsnLeuLeuGlnGlyTyrAla 120
Db 1872 GCGCGTCTTTTATCCAGAGATGATTTATGTCAGAC---ATTATGCTGTTATGC 1928
QY 120 AlaTyrArgTyrAlaGlnProThrProAlaThrAlaAlaTyrSerAspSer----- 138
Db 1929 TGCATACCGCTACGCGCCAGCTACCTCGCACCTGCGCTACAGTACAG-AAATC 1987
QY 139 -----TyrGlyArgVa 142
Db 1988 AGTTCGCTCTGCTGACGACGAGTAAATTTCTGTAAACCTCTGCACTTACGAGCAGT 2047
QY 142 1TYrAlaAlaAspProTyr 148
Db 2048 TTATGCTGCCGACCCCTAC 2066

RESULT 2

US-09-176-657-5
; Sequence 5, Application US/09176657
; Patent No. 6020164
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/176,657
; CURRENT FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-09-176-657-5

Alignment Scores:

Pred. No.: 1,92e-29 Length: 1506
Score: 379.00 Matches: 86
Percent Similarity: 59.63% Conservative: 10
Best Local Similarity: 53.42% Mismatches: 37
Query Match: 47.61% Indels: 29
DB: 3 Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-176-657-5 (1-1506)

QY 1 MetThrAsnLysLysAlaValAsnProTyrThrAsnGlyTyrPlySLeuAsnProValVal 20
Db 768 ATGACCAATAGAGATGTGTACACCATATGCAATGTTGGAAATTAAGCCAGTGT 827
QY 21 G1YAlaValTyrSerProaepheTyrAlaGlyThrValLeuLeuCySGlnAlaAsn--- 39

Db 828 GAGAGCTATATGCTCCGAGATATATGACGATCCAGCTTTCACAGATGTGTCCCTTA 887
QY 40 ---GlnGluGlySerSermetTyrSerGlyProSerSerLeu-----ValTyrThrSer 56
Db 888 GGCATATGACGACGATGCTCCCTATACGAGAAGGGGGTATCAACCTTATCTCTTA 947
QY 57 AlaMetProGlyPheProTyrPro---AlaAlaThrAlaAlaAlaTyrArgGlyAla 75
Db 948 ATCATTCCTGGCTTCTCCCTTACCTACTGACGACACGCGAGCGCTTTCAGAGAGCC 1007
QY 76 HisLeuArgGlyArgGlyArgThrValTyrAsnThrPheArgAlaAlaAlaProPro 95
Db 1008 CATTTAGGGGCGAGAGCGGCGACAGTATGTGTACGTCCGA---GCGGTACCTCCACAA 1064
QY 96 ProIleProAlaTyrGlyValValTyrGlnGluProValTyrGlyAsnLeuLeu 115
Db 1065 GCCATCCCGCTATC----- 1081
QY 116 GlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
Db 1082 AGCGGTGATATGACAGCTTACAGATATGACAGCTGCTACGCAACCGAGCCAGCT 1141
QY 132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAspPro 147
Db 1142 GCTGACCGCGCTGACGCGCTTACGTATGACGTTATGCGAGGGGTATACACAGCCGCC 1201
QY 148 Tyr 148
Db 1202 TAC 1204

RESULT 3

US-09-421-299-5
; Sequence 5, Application US/09421299
; Patent No. 6524579
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Lu, Alina
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/421,299
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: 09/176,657
; EARLIER FILING DATE: 1998-10-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 1506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1250374
US-09-421-299-5

Alignment Scores:

Pred. No.: 1,92e-29 Length: 1506
Score: 379.00 Matches: 86
Percent Similarity: 59.63% Conservative: 10
Best Local Similarity: 53.42% Mismatches: 37
Query Match: 47.61% Indels: 29
DB: 4 Gaps: 6

US-09-809-545a-2_COPY_1_148 (1-148) x US-09-421-299-5 (1-1506)

QY 1 MetThrAsnLysLysAlaValAsnProTyrThrAsnGlyTyrPlySLeuAsnProValVal 20
Db 768 ATGACCAATAGAGATGTGTACACCATATGCAATGTTGGAAATTAAGCCAGTGT 827
QY 21 G1YAlaValTyrSerProaepheTyrAlaGlyThrValLeuLeuCySGlnAlaAsn--- 39

```

Db      828 GGAGCTGATATGTCGCGAGTTATATGCAATCCAGCTTTACAGAGATGTCCTTA 887
      40 ---GlnGlnGlySerMetTyrserylProSerSeru-----ValTyrThrser 56
      888 GCGAATGATCAGCAGAGCCCTTATCAGAGAGGGGGATTCACACTTATTCCTTTA 947
      57 AlameProglYpneProTyPro---AlaAlaThrAlaAlaAlaAlaAlaAlaAla 75
      948 ATCATTCCTGCTTCCCTTATCCTTACGAGCCACGACCGCCTTTTCAAGAGGCC 1007
      76 HisLeuArgGlyArgGlyArgGlyValTyrAsnThrPheArgAlaAlaAlaProPro 95
      1008 CATTGAGGGGAGAGGGCGCAGATATGTCAGTCCGA---CGGTACCTCCCAACA 1064
      96 ProIleProAlaTyrGlyGlyValValTyrGlnGluProAlaTyrGlyAsnLysLeuLeu 115
      1065 GCCATCCCGCGCTATCC----- 1081
      116 GlnGlyGlyTyrAlaAlaTyrArgTyrAlaGlnProThrProAlaThr----- 131
      1082 AGGGGTGGATATGAGCTTACAGATATGCAAGCTGCTACTGCAACCGCAGCCGCT 1141
      132 -----AlaAlaAlaTyrSerAspSerTyrGlyArgValTyrAlaAlaAlaPro 147
      1142 GCTGACGCCGCTGACGCGCTTACAGTACGAGTTATGCGGGGTGTACACAGCCGACCC 1201
      148 Tyr 148
      1202 TAC 1204
  
```

RESULT 4

```

US-08-935-450-10
; Sequence 10, Application US/08935450
; Patent No. 5977311
; GENERAL INFORMATION:
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Yang, Meljia
; APPLICANT: Schulz, Vincent
; TITLE OF INVENTION: 53BP2 COMPLEXES
; FILE REFERENCE: 7934-054
; CURRENT APPLICATION NUMBER: US/08/935,450
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 914
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-935-450-10
  
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Alignment Scores:

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Pred. No.: 1          Length: 914
Score: 93.00         Matches: 39
Percent Similarity: 41.38%      Conservative: 9
Best Local Similarity: 33.62%    Mismatches: 42
Query Match: 11.68%            Indels: 26
DB: 2                      Gaps: 5
  
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US-09-809-545a-2_COPY_1_148 (1-148) x US-08-935-450-10 (1-914)

```

QY      24 TyrserylProAspSerTyrserylValValLeuLeuGlnAlaGlnGlnGlnGlnGln 43
      230 TACAGCCCT-----GCTCGAATCCCGCCAGAGGCC 259
      44 SerMetTyrserylProSerSerLeuValTyrThrSerAla-MetProglYpneProTy 63
      260 AGACCTTACATATGAAGACCAATCCCTGCTCAAGCCCAATACACACCCACCC 319
      63 rProAlaAlaThrAla-----AlaAlaAlaTyrArgGlyAlaHisLeuArgGlyArgG 81
      320 GTGAGCAGTACAGCCCTTCCACAGCCGAGTTACAGCCACCACTTAC---AACAGAG 376
  
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QY      81 yArgThrValTyrAsnThrPheArgAlaAlaAla-ProProProProIleProAlaTyr 101
      377 GAGTTTACAGCAGAGGTTTACACAGCCCACTTCCACCTTCCACACACCTGCTTCA 436
      101 LysGlyValValTyrGlnGlnProValTyrGlyAsnLysLeuLeuGlnGlnGlnGln 121
      437 AC-----TATGGAGC-----TACGGGGTTACAMCC 463
      121 LysTyrArgTyrAlaGlnProThrProAlaThrAlaAlaAlaTyr 135
      464 CGGCCCTTATACCCACCCGACCCGACCCGACCCGACAGACTTAC 507
  
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RESULT 5

```

US-08-258-261B-6
; Sequence 6, Application US/08258261B
; Patent No. 5639949
; GENERAL INFORMATION:
; APPLICANT: Schnupp, Thomas
; APPLICANT: Ligot, James M.
; APPLICANT: Beck, James Joseph
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Gaffney, Thomas Deane
; APPLICANT: Lam, Stephen Ting
; APPLICANT: Hammer, Phillip E.
; APPLICANT: Uknes, Scott Joseph
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/258,261B
; FILING DATE: 08-JUN-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/457,205
; FILING DATE: 01-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rimer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET INFORMATION: CGC 1506/CIP3
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28958 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
  
```

Alignment Scores:

```

Pred. No.: 106          Length: 28958
Score: 92.50           Matches: 34
Percent Similarity: 41.28%      Conservative: 11
Best Local Similarity: 31.19%    Mismatches: 52
Query Match: 11.62%            Indels: 12
DB: 1                      Gaps: 4
  
```



```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,342
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-457-342-6

```

```

Alignment Scores:
Pred. No.: 106          Length: 28958
Score: 92.50           Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62%      Indels: 12
DB: 1                  Gaps: 4

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US-09-809-545a-2_COPY_1_148 (1-148) x US-08-457-342-6 (1-28958)

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QY 47 SerGlyProSerSerLeuValTyThrSerAlaMetProGlyPheProTyRProAlaAla 66
DB 10706 AGCGGCTCTCCGACGATGGGCGATCGCTTCCGTCGAGGTCAGCCCGCCATCCCGTCTCA 10765
QY 67 ThrAlaAlaAlaAlaTyR--ArgGlyAlaHis-LeuArgGlyAArgGlyAArgThyValTy 85
DB 10766 CGCTCCGCTCCGCGGACCTCGGAGCGCTCACCGCTCGATCCGCTGTCGCGCTCCA 10825
QY 85 rAntThrPheArgAlaAlaAlaProProProProIleProAlaTyRgIyValValTy 105
DB 10826 TTCGACG--AGAGAGAGGCGCACCTCGCCGCTGCTCTCTCGGGCGAGCTCTCTA 10882
QY 105 rGIngluProValTyRgIyAsnlySLeuGIngluGlyTyRAlaAlaTyRgTyRAl 125
DB 10883 CCGGAGGCT-----CGCGCTCGACTGAGAGGACTTCTTCGCGCCCTACGCTCCCC 10933
QY 125 agIn-----ProThrProAlaThrAlaAlaAlaTyRserAspSerTy 139
DB 10934 GCAAGCTCTCCCTCCACCTACCCCTTCCAGGAGAGCGGTTCTGCTCGAGTCTCCA 10993
QY 139 rGlyArgValTyRAlaAlaAspPro 147
DB 10994 CGGACGAAAGCTTCCGACGTCGCT 11018

```

RESULT 8

```

US-08-457-646a-6
Sequence 6, Application US/08457646a
Patent No. 5679560
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting

```

```

APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,646a
FILING DATE: 01-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457,205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258,261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-457-646a-6

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Alignment Scores:

```

Pred. No.: 106          Length: 28958
Score: 92.50           Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62%      Indels: 12
DB: 1                  Gaps: 4

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US-09-809-545a-2_COPY_1_148 (1-148) x US-08-457-646a-6 (1-28958)

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QY 47 SerGlyProSerSerLeuValTyThrSerAlaMetProGlyPheProTyRProAlaAla 66
DB 10706 AGCGGCTCTCCGACGATGGGCGATCGCTTCCGTCGAGGTCAGCCCGCCATCCCGTCTCA 10765
QY 67 ThrAlaAlaAlaAlaTyR--ArgGlyAlaHis-LeuArgGlyAArgGlyAArgThyValTy 85
DB 10766 CGCTCCGCTCCGCGGACCTCGGAGCGCTCACCGCTCGATCCGCTGTCGCGCTCCA 10825
QY 85 rAntThrPheArgAlaAlaAlaProProProProIleProAlaTyRgIyValValTy 105
DB 10826 TTCGACG--AGAGAGAGGCGCACCTCGCCGCTGCTCTCTCGGGCGAGCTCTCTA 10882
QY 105 rGIngluProValTyRgIyAsnlySLeuGIngluGlyTyRAlaAlaTyRgTyRAl 125
DB 10883 CCGGAGGCT-----CGCGCTCGACTGAGAGGACTTCTTCGCGCCCTACGCTCCCC 10933
QY 125 agIn-----ProThrProAlaThrAlaAlaAlaTyRserAspSerTy 139
DB 10934 GCAAGCTCTCCCTCCACCTACCCCTTCCAGGAGAGCGGTTCTGCTCGAGTCTCCA 10993

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Qy 139 rgiArgValTyraAlaAlaaspPro 147
Db 10994 CGACGACGCTTCGACGCTGCTT 11018

RESULT 9
US-08-458-076A-6
Sequence 6, Application US/08458076A
Patent No. 5696425
GENERAL INFORMATION:
APPLICANT: Schnupp, Thomas
APPLICANT: Ligon, James M.
APPLICANT: Beck, James Joseph
APPLICANT: Hill, Dwight Steven
APPLICANT: Ryals, John Andrew
APPLICANT: Gaffney, Thomas Deane
APPLICANT: Lam, Stephen Ting
APPLICANT: Hammer, Phillip E.
APPLICANT: Uknes, Scott Joseph
TITLE OF INVENTION: Genes for the synthesis of
TITLE OF INVENTION: antipathogenic substances
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458, 076A
FILING DATE: 01-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/457, 205
FILING DATE: 01-JUN-1995
APPLICATION NUMBER: 08/258, 261
FILING DATE: 08-Jun-1994
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-458-076A-6

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545a-2_COPY_1_148 (1-148) x US-08-458-076A-6 (1-28958)

Qy 47 SerGlyProSerSerLeuValTyThrSerAlaMetProGlyPheProTyProAlaAla 66
|||||
|||||

Db 10706 AGCGGCTCTCGACGATGGGATCGCTTCCTCGAGGTCAAGCCCCATCCGCTCTCA 10765
Qy 67 ThrAlaAlaAlaAlaTyrr--ArgGlyAlaHis-LeuArgGlyArgGlyThrValTy 85
Db 10766 CGCTCCGCTCCGCGAGACCTGGAGCGCTCAACGCTCGATCCGCTCGTGTGGCTCCA 10825
Qy 85 rAenthPheArgAlaAlaAlaAlaProProProPolleProAlaTyrglyValValTy 105
Db 10826 TTCGACG---AGAAAGAGCCACCTCGCCGCTCTCTCTCTCTGCGGCGAGCTCTCA 10882
Qy 105 rGlnGluProValTyrglyValAsnlybLeuGlnGlnGlyTyraAlaAlaTyrrArgTyAl 125
Db 10883 CCGAGGCTT-----CGCGCTGACTGGAAGGACTTCTTGGCGCTTACGCTCCCC 10933
Qy 125 agln-----ProThrProAlaThrAlaAlaAlaAlaTyrrSerAspSerTy 139
Db 10934 GCAAGGTCCTCCCTCCCACTACCTCTTCCAGGAGAGGGGTTCGTGGCTCGAGCTCCCA 10993
Qy 139 rgiArgValTyraAlaAlaaspPro 147
Db 10994 CGACGACGCTTCGACGCTGCTT 11018

RESULT 10
US-08-764-233A-4
Sequence 4, Application US/08764233A
Patent No. 5716849
GENERAL INFORMATION:
APPLICANT: Schnupp, Thomas
APPLICANT: Beck, James J.
APPLICANT: Hill, Dwight S.
APPLICANT: Neff, Snezana
APPLICANT: Ryals, John A.
TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764, 233A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729, 214
FILING DATE: 09-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258, 261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 1506/CIP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Sorangium cellulosum

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: IMMEDIATE SOURCE:
: CLONE: p98/1
US-08-764-233A-4

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545A-2_COPY_1_148 (1-148) x US-08-764-233A-4 (1-28958)
QY 47 SerGlyProSerSerLeuValTyThrSerAlaMetProGlyPheProTyProAlaAla 66
Db 10706 AGCGGCTCTCGACGATGGGATCGCTTCTCCGTCGAGTCAGACCCCATCCGCTCTCA 10765
QY 67 ThrAlaAlaAlaAlaTyR---ArgGlyAlaHis-LeuArgGlyArgGlyArgThyValTy 85
Db 10766 CGCTGCGCCCTCGGAGACCTGCGAGCGCTCACCGCTGATCCCGTGTGTCGCTCCA 10825
QY 85 AsnThrPheArgAlaAlaAlaProProProIleProAlaTyGlyGlyValValTy 105
Db 10826 TTCACG---AGAAGAAGCCACCTCCGCCCTCTCTCTCTGCGGCGAGCTCTTCA 10882
QY 105 rGlnGluProValTyGlyAsnTybLeuLeuGlnGlyGlyTyAlaAlaAlaTyArgTyAl 125
Db 10883 CCCGAGGCGCT-----CGCGCTCGACGAAAGACTTCTTCCGCGCCCTACGCTCCCC 10933
QY 125 aGln-----ProThrProAlaThrAlaAlaAlaTySerAspSerTy 139
Db 10934 GCAAGGTCCTCCCTCCCACTTACCCCTTCACGAGCGGGTTCGGCTCGACGTCCTCA 10993
QY 139 rGlyArgValTyAlaAlaAlaPro 147
Db 10994 CGGACGAACGCTTCCGACGTCGCT 11018

RESULT 11
US-08-457-335A-6
: Sequence 6, Application US/08457335A
: Patent No. 5723759
: GENERAL INFORMATION:
: APPLICANT: Schupp, Thomas
: APPLICANT: Ligon, James M.
: APPLICANT: Beck, James Joseph
: APPLICANT: Hill, Dwight Steven
: APPLICANT: Ryals, John Andrew
: APPLICANT: Gaffney, Thomas Deane
: APPLICANT: Lam, Stephen Ting
: APPLICANT: Hammer, Phillip E.
: APPLICANT: Ukens, Scott Joseph
: TITLE OF INVENTION: Genes for the synthesis of
: TITLE OF INVENTION: antipathogenic substances
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ciba-Geigy Corporation
: STREET: 7 Skyline Drive
: CITY: Hawthorne
: STATE: NY
: COUNTRY: USA
: ZIP: 10532
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/457,335A
: FILING DATE: 01-JUN-1995
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/457,205

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/ FILING DATE: 01-JUN-1995
/ APPLICATION NUMBER: 08/258,261
/ FILING DATE: 08-Jun-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Elmer, James Scott
/ REGISTRATION NUMBER: 36,129
/ REFERENCE/DOCKET NUMBER: CGC 1506/CIP3
/ TELEPHONE: 919-541-8614
/ TELEFAX: 919-541-8689
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 28958 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHEetical: NO
/ ANTI-SENSE: NO
US-08-457-335A-6

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545A-2_COPY_1_148 (1-148) x US-08-457-335A-6 (1-28958)

OY 47 SerGlyProSerSerLeuValTyrThrSerAlaMetProGlyPheProTyrProAlaAla 66
Db 10706 AGCGGCTCCCTCGACGATGCGCATCGCTCTCCGTCGAGGTCAAGCCCTCCATCCGTCGCTCA 10765
OY 67 ThrAlaAlaAlaAlaTyr---ArgGlyAlaHis-LeuArgGlyArgGlyArgThrValTyr 85
Db 10766 CGCTCGCCCTCCCGAGACCTCGAGCGCTCACCGCTCATCCGTCGTCGCTCGCTCA 10825
OY 85 PAsnThrPheArgAlaAlaAlaProProProProleProAlaTyrGlyGlyValValTyr 105
Db 10826 TTCGACG---AGAAAGAGCGCACCTCGCCCGCTGCTCTCTTCCTCGGAGAGCTCTCA 10882
OY 105 rGIngluProValTyrGlyValAsnLysLeuLeuGInglYrTyrAlaAlaTyrArgTyrAl 125
Db 10883 CCGAGGCGCT-----CGCGCTCGACTGGAAGACTTTCGCGCGCTACGCTCCCC 10933
OY 125 aGIn-----ProThrProAlaThrAlaAlaAlaTyrSerAspSerTyr 139
Db 10934 GCAAGGCTCCCTCCGCCACCTACCCCTTCGACGAGAGCGGTTCTGCTCGACGTCTCCA 10993
OY 139 rGlyArgValTyrAlaAlaAspPro 147
Db 10994 CGGACGAAAGCTTCGACGTCGCT 11018

RESULT 12
US-08-729-214-6
/ Sequence 6, Application US/08729214
/ Patent No. 5817502
/ GENERAL INFORMATION:
/ APPLICANT: Ligon, James M.
/ APPLICANT: Hill, Dwight Steven
/ APPLICANT: Ryals, John Andrew
/ APPLICANT: Hammer, Phillip E.
/ APPLICANT: van Pee, Karl-Heinz
/ APPLICANT: Kirner, Sabine
/ TITLE OF INVENTION: Genes for the synthesis of
/ TITLE OF INVENTION: antipathogenic substances
/ NUMBER OF SEQUENCES: 27
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Ciba-Geigy Corporation
/ STREET: 520 White Plains Road
/ CITY: Yarritytown
/

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STATE: NY  
COUNTRY: USA  
ZIP: 10591
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPILER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,214
FILING DATE: TBA
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1506/CIPS
TELECOMMUNICATIONS INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 28958 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-729-214-6

Alignment Scores:
Pred. No.: 106 Length: 28958
Score: 92.50 Matches: 34
Percent Similarity: 41.28% Conservative: 11
Best Local Similarity: 31.19% Mismatches: 52
Query Match: 11.62% Indels: 12
DB: 1 Gaps: 4

US-09-809-545A-2_COPY_1_148 (1-148) x US-08-729-214-6 (1-28958)

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Oy      67 ThrIlaIalaaIatYr---ArgGlYaIahie-LeuaRGgLYARGLYAARGThrVaLy 85
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Db     10766 CCGTCGCCCTCCGGAGAAGACTGCGAGGGCTCACCGCTCGATCCCGRCTGRTGAGCTCCA 108255
Oy      85 rAsnTrhPhearGYaIIaIaaIPRoPRoPRoPolleIRPoLaITyrGlglyaIVaLVaLy 105
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Db     10883 CCCGAGGCT-----CGCGCTGACTGGAAGAATTCTTGGGGCCCTTAGCTCCCC 109333
Oy      125 agLI-----ProthrPROlatrhIAIaaIAtYrsEraspsERTy 139
        |::|
Db     10934 GCAGAGCTCCCTCCCACTACCTTCCAGAGAGCGGTTCTGGCTCGACGTCTCCA 109933
Oy      139 rGLYArgVAlTYraIaaIaaSPRO 147
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Db     10994 CGGACGAACGCTTCCGAGCTCGCT 11018
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RESULT 13
US-09-028-934-6
Sequence 6, Application US/09028934
Patent No. 6117670
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Hill, Dwight S.
APPLICANT: Lam, Steven T.
APPLICANT: Hammer, Philip E.

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1  APPLICANT: van Pee, Karl-Heinz
2  APPLICANT: Kliner, Sabine
3  APPLICANT: Young, Thomas R.
4  TITLE OF INVENTION: Pyrolytic Biosynthesis Genes and Uses
5  TITLE OF INVENTION: Thereof
6  NUMBER OF SEQUENCES: 37
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: No. 611767artis Corporation
9  STREET: 3054 Cornwallis Road
10 CITY: Research Triangle Park
11 STATE: NC
12 COUNTRY: USA
13 ZIP: 27709
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: PatentIn Release #1.0, Version #1.30
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/028,934
21 FILING DATE:
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 08/729,214
25 FILING DATE: 09-OCT-1996
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 08/258,261
28 FILING DATE: 08-JUN-1994
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Meigs, J. Timothy
31 REGISTRATION NUMBER: 38,241
32 REFERENCE/DOCKET NUMBER: CGC1506/CIP7
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 919-541-8567
35 TELEFAX: 919-541-8689
36 INFORMATION FOR SEQ ID NO: 6:
37 SEQUENCE CHARACTERISTICS:
38 LENGTH: 28958 base pairs
39 TYPE: nucleic acid
40 STRANDEDNESS: single
41 TOPOLOGY: linear
42 MOLECULE TYPE: DNA (genomic)
43 HYPOTHEICAL: NO
44 ANTI-SENSE: NO
45 US-09-028-934-6
46
47 Alignment Scores:
48 Pred. NO.: 106 Length: 28958
49 Score: 92.50 Matches: 34
50 Percent Similarity: 41.28% Conservative: 11
51 Best Local Similarity: 31.19% Mismatches: 52
52 Query Match: 11.62% Indels: 12
53 DB: 3 Gaps: 4
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55 US-09-809-545A-2_COPY_1_148 (1-148) x US-09-028-934-6 (1-28958)
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57 47 SerGlyProSerSerIleuValTYrThrSerAlaMetProGlyPheProTYrProAlaAla 66
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59 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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61
62 67 ThrAlaAlaAlaAlaTYr--ArgGlyAlaHis-LeuArgGlyArgGlyArgThrValTY 85
63 ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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67 85 rAsnThrPheArgAlaAlaAlaProProProPoleProAlaTYrGlyGlyValValTY 105
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70 TTCACG---AGAAAGAGCGCACCTCGCCGCTGCTCCTCCTCGGGGAGACTCTCA 108822
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72 105 rGlnGlnProValTYrGlyAsnIleuGlnGlnGlyTYrAlaAlaTYrArgTYrAl 125
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77 125 agln-----ProthrProAlaThrAlaAlaAlaTYrSerAspSerTY 139

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Db 10934 GCAAGCTCTCCCTCCACCTACCCCTTCCAGCAGACGCGTTCGCTGACGTCCTCA 10993
Qy 139 rglaryvaltyrAlaAlaAspPro 147
Db 10994 CGAGCGAACGCTTCGACGTCGCT 11018

RESULT 14
US-08-764-233A-1
Sequence 1, Application US/08764233A
Patent No. 5716849
GENERAL INFORMATION:
APPLICANT: Ligon, James M.
APPLICANT: Beck, James J.
APPLICANT: Hill, Dwight S.
APPLICANT: Neff, Snezana
APPLICANT: Ryals, John A.
TITLE OF INVENTION: Genes For The Biosynthesis Of Soraphen
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: NY
COUNTRY: USA
ZIP: 10591

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,233A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/729,214
FILING DATE: 09-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/258,261
FILING DATE: 08-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 1506/CIP6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 49377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: Sorangium cellulosum
IMMEDIATE SOURCE:
CLONE: p98/1, pLJ3, and pVKM15
FEATURE:
NAME/KEY: misc feature
LOCATION: 383_760
OTHER INFORMATION: /product= "SorA"
OTHER INFORMATION: /note= "This gene encodes a protein that is highly homologous
OTHER INFORMATION: the reductase domains of type I PKSs such as eryA from
OTHER INFORMATION: Saccharopolyspora erythraea."
FEATURE:
NAME/KEY: misc feature
LOCATION: 927_19874
OTHER INFORMATION: /product= "SorA"
OTHER INFORMATION: /note= "Gene product is highly homologous to type I PKSs that
OTHER INFORMATION: are known to be involved in the synthesis of polyketide

OTHER INFORMATION: compounds."
FEATURE:
NAME/KEY: misc feature
LOCATION: 942_7115
OTHER INFORMATION: /product= "Module 1 of SorA"
FEATURE:
NAME/KEY: misc feature
LOCATION: 7203_12884
OTHER INFORMATION: /product= "Module 2 of SorA"
FEATURE:
NAME/KEY: misc feature
LOCATION: 13455_19616
OTHER INFORMATION: /product= "Module 3 of SorA"
FEATURE:
NAME/KEY: misc feature
LOCATION: 19870_46318
OTHER INFORMATION: /product= "SorB"
OTHER INFORMATION: /note= "gene product is highly homologous to type I PKS gene"
FEATURE:
NAME/KEY: misc feature
LOCATION: 19870_24556
OTHER INFORMATION: /product= "Module 1 of SorB"
FEATURE:
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LOCATION: 24638_30820
OTHER INFORMATION: /product= "Module 2 of SorB"
FEATURE:
NAME/KEY: misc feature
LOCATION: 30881_35446
OTHER INFORMATION: /product= "Module 3 of SorB"
FEATURE:
NAME/KEY: misc feature
LOCATION: 35528_40114
OTHER INFORMATION: /product= "Module 4 of SorB"
FEATURE:
NAME/KEY: misc feature
LOCATION: 40190_46318
OTHER INFORMATION: /product= "Module 5 of SorB"
FEATURE:
NAME/KEY: misc feature
LOCATION: 46851_47891
OTHER INFORMATION: /product= "SorM"
OTHER INFORMATION: /note= "The protein encoded by the sorM gene is highly
OTHER INFORMATION: homologous to the methyltransferase from Streptomyces
OTHER INFORMATION: hygroscopicus that is involved in the synthesis of the
OTHER INFORMATION: polyketide rapamycin."

US-08-764-233A-1

Alignment Scores:
Pred. No.: 214
Score: 92.50
Percent Similarity: 41.284
Best Local Similarity: 31.198
Query Match: 11.624
DB: 1
Length: 49377
Matches: 34
Conservative: 11
Mismatch: 52
Indels: 12
Gaps: 4

US-09-809-545A-2_copy_1_148 (1-148) x US-08-764-233A-1 (1-49377)

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Qy 67 ThrAlaAlaAlaAlaTyThrArgGlyAlaHis-LeuArgGlyArgGlyThrValTy 85
Db 27069 CGCTGCCCTCGCGAGACCTCGAGCGCTCAACGCTCATCCGTCGTCGCTCA 27128
Qy 85 rAsnThrPheArgAlaAlaAlaProProProProAlaTyArgGlyValValTy 105
Db 27129 TTCAGCG--AGAAAGAGCACCCTCGCGCTGCTCTCTCCGCGGAGAGCTCTCA 27185
Qy 105 rGlnGluProValTyrGlyAsnLysLeuLeuGlnGlyGlyTyrrAlaAlaTyrrArgTyrrAl 125
Db 27186 CCGGAGCGCT-----CGCGCTCGACTGGAAGACTTTCGCGCCCTCAAGCTCCCC 27236

Qy	125	agln-----	-ProthrProAlathrAlaAlaAlaTysSerasperty	139
Db	27237	GCAGGCTCTCCCTCCCAACCTACCCCTTCCAGGAGAGCGGCTTCTGGCTCGACGTCTCCA		27296
Qy	139	rglYargvalYrAlaAlaAlaAspPro		147
Db	27297	CGGAGGAAAGCTTCCGACGTCGCTT	27321	

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US-08-990-823-62
RESULT 15
Sequence 62: Application US/08990823D
Patent No. 6228371
GENERAL INFORMATION:
APPLICANT: Nano, Francis
TITLE OF INVENTION: Mycobacterium Tuberculosis DNA Sequences Encoding
TITLE OF INVENTION: Immunostimulatory Peptides
FILE REFERENCE: 49086
CURRENT APPLICATION NUMBER: US/08/990,823D
CURRENT FILING DATE: 1997-12-15
EARLIER APPLICATION NUMBER: US 96/10375
EARLIER FILING DATE: 1996-06-14
EARLIER APPLICATION NUMBER: 60/000,254
EARLIER FILING DATE: 1995-06-15
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 62
LENGTH: 821
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
NAME/KEY: Modified base
OTHER INFORMATION: n represents a or g or c or t/u
US-08-990-823-62

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Alignment Scores:	
Pred. No.:	1.39
Score:	91.00
Percent Similarity:	90.85%
Best Local Similarity:	23.94%
Query Match:	11.43%
DB:	3
length:	822
Matches:	45
Conservative:	13
Mismatches:	76
Indels:	5
Gaps:	64

US-09-809-545A-2_COPY_1_148 (1-148) X US-08-990-823-62 (1-821)

[illegible]

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QY      106  GlnGluProValTyrGlyValAsnLys-----LeuLeuGlnGlyValY-----118
Db      481  -----GTTTTCGGCGGCGCGGCACATCTGGTCTTACAGAGAGACGGCGATTTCATCTA 534
QY      119  -----TyrAlaIaTyrArgTyrAlaGlnProThrProIaThr 131
Db      535  CGGCGCACTCCCTGAACCTGCAGTGGGGGGCTACCGCGCGGACGGCGCATTCAGCCACT 594
QY      132  AlaAlaIaTyrSerAspSerTyr 139
Db      595  GGGGCAAGTATTTCCGATCGACACT 618

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Search completed: January 15, 2004, 09:59:35
Job time : 103.912 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: January 30, 2004, 16:58:29 ; Search time 21 Seconds
(without alignments)
298.191 Million cell updates/sec

Title: US-09-809-545a-2_COPY_1_148
Perfect score: 148
Sequence: 1 MTNKKAVNPYINGWKLNPV.....PATMAAYSDSYGRVAAADPY 148

Scoring table: OLIGO
Gapop 60.0 , Gapept 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents_Aa: *
1: /cgn2_6/ptodata/1/1aa/5A COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	57	38.5	330	3	US-09-145-391-2	Sequence 2, Appl1
2	13	8.8	366	3	US-09-176-657-2	Sequence 2, Appl1
3	13	8.8	366	4	US-09-421-299-2	Sequence 2, Appl1
4	8	5.4	325	4	US-09-702-705-1816	Sequence 1816, Ap
5	8	5.4	325	4	US-09-736-457-1816	Sequence 1816, Ap
6	8	5.4	342	3	US-09-043-937A-2	Sequence 2, Appl1
7	8	5.4	882	3	US-09-413-814-78	Sequence 78, Appl
8	7	4.7	7	2	US-08-666-473-13	Sequence 13, Appl
9	7	4.7	11	2	US-07-814-220-5	Sequence 5, Appl1
10	7	4.7	11	2	US-07-812-421-5	Sequence 5, Appl1
11	7	4.7	11	4	US-09-117-121-2	Sequence 2, Appl1
12	7	4.7	20	2	US-07-814-220-27	Sequence 27, Appl
13	7	4.7	20	2	US-07-812-421-27	Sequence 27, Appl
14	7	4.7	21	2	US-07-814-220-24	Sequence 24, Appl
15	7	4.7	21	2	US-07-812-421-24	Sequence 24, Appl
16	7	4.7	25	2	US-07-814-220-33	Sequence 33, Appl
17	7	4.7	25	2	US-07-812-421-33	Sequence 33, Appl
18	7	4.7	28	2	US-07-814-220-36	Sequence 36, Appl
19	7	4.7	28	2	US-07-812-421-36	Sequence 36, Appl
20	7	4.7	33	4	US-09-117-121-3	Sequence 3, Appl1
21	7	4.7	38	4	US-09-117-121-16	Sequence 16, Appl
22	7	4.7	38	4	US-09-117-121-24	Sequence 24, Appl
23	7	4.7	38	4	US-09-117-121-26	Sequence 26, Appl
24	7	4.7	38	4	US-09-344-529-5	Sequence 5, Appl1
25	7	4.7	39	4	US-09-117-121-18	Sequence 18, Appl
26	7	4.7	39	4	US-09-117-121-20	Sequence 20, Appl
27	7	4.7	39	4	US-09-117-121-22	Sequence 22, Appl

28	7	4.7	39 4	US-09-117-121-28	Sequence 28, Appl
29	7	4.7	39 4	US-09-117-121-32	Sequence 32, Appl
30	7	4.7	39 4	US-09-117-121-35	Sequence 35, Appl
31	7	4.7	39 4	US-09-117-121-36	Sequence 36, Appl
32	7	4.7	54 4	US-09-117-121-30	Sequence 30, Appl
33	7	4.7	63 2	US-08-700-013B-2	Sequence 2, Appl1
34	7	4.7	63 2	US-08-700-013B-4	Sequence 4, Appl1
35	7	4.7	76 6	5496550-6	Patent No. 5496550
36	7	4.7	96 3	US-08-465-343A-11	Sequence 11, Appl
37	7	4.7	98 2	US-07-814-220-11	Sequence 2, Appl1
38	7	4.7	98 2	US-07-812-421-2	Sequence 2, Appl1
39	7	4.7	105 4	US-09-191-468-104	Sequence 104, App
40	7	4.7	105 4	US-09-191-468-106	Sequence 106, App
41	7	4.7	105 4	US-09-191-468-108	Sequence 108, App
42	7	4.7	105 4	US-09-191-468-110	Sequence 110, App
43	7	4.7	105 4	US-09-191-468-112	Sequence 112, App
44	7	4.7	105 4	US-09-191-468-114	Sequence 114, App
45	7	4.7	105 4	US-09-191-468-116	Sequence 116, App

ALIGNMENTS

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RESULT 1
US-09-145-391-2
; Sequence 2, Application US/09145391
; Patent No. 6194171
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; APPLICANT: Shibata, Hiroki
; TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
; FILE REFERENCE: CE 3093
; CURRENT FILING DATE: 1998-09-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-145-391-2

Query Match      38.5%; Score 57; DB 3; Length 330;
Best Local Similarity 100.0%; Pred. No. 2.1e+49;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      49 PSSLVYTSAMPGEPPYPAATMAAAYRGAAHLRGGRVTYNTFRRAAPPPIPAYGVVY 105
Db      244 PSSLVYTSAMPGEPPYPAATMAAAYRGAAHLRGGRVTYNTFRRAAPPPIPAYGVVY 300

RESULT 2
US-09-176-657-2
; Sequence 2, Application US/09176657
; Patent No. 6020164
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Tang, Y. Tom
; APPLICANT: Corley, Neil C.
; APPLICANT: Guejler, Karl J.
; APPLICANT: Lu, Aina
; TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
; FILE REFERENCE: PF-0611 US
; CURRENT APPLICATION NUMBER: US/09/176, 657
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Homo sapiens
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FEATURE: -
OTHER INFORMATION: 1250374
US-09-176-657-2

Query Match 8.8%; Score 13; DB 3; Length 366;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 RGATLRGRGRTVY 85
DB 267 RGATLRGRGRTVY 279

RESULT 3
US-09-421-299-2
Sequence 2, Application US/09421299

PATENT NO. 6524579
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Lu, Anna
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PF-0611 US
CURRENT APPLICATION NUMBER: US/09/421,299
CURRENT FILING DATE: 1999-10-20
EARLIER APPLICATION NUMBER: 09/176,657
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 366
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: -
OTHER INFORMATION: 1250374
US-09-421-299-2

Query Match 8.8%; Score 13; DB 4; Length 366;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 RGATLRGRGRTVY 85
DB 267 RGATLRGRGRTVY 279

RESULT 4
US-09-702-705-1816
Sequence 1816, Application US/09702705
PATENT NO. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1816
LENGTH: 325
TYPE: PRT

ORGANISM: Homo sapiens
US-09-702-705-1816

Query Match 5.4%; Score 8; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 AAAPPPI 97
DB 67 AAAPPPI 74

RESULT 5
US-09-736-457-1816
Sequence 1816, Application US/09736457

PATENT NO. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1816
LENGTH: 325
TYPE: PRT
ORGANISM: Homo sapiens
US-09-736-457-1816

Query Match 5.4%; Score 8; DB 4; Length 325;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 AAAPPPI 97
DB 67 AAAPPPI 74

RESULT 6
US-09-043-937A-2
Sequence 2, Application US/09043937A
PATENT NO. 6211432
GENERAL INFORMATION:
APPLICANT: BOUDET, ALAIN-MICHEL
PICHON, MAGALIE
GRIMA-PETEMATI, JACQUELINE
BECKERT, MICHEL
GAMAS, PASCAL
BRIAT, JEAN-FRANCOIS
TITLE OF INVENTION: DNA SEQUENCES CODING FOR CINNAMOYL-CoA
REDUCTASE, AND APPLICATIONS THEREOF IN THE CONTROL OF
LIGNIN CONTENTS IN PLANTS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE, P.C.
STREET: 110 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/043,937A
FILING DATE: 24-Jul-1998
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR96/01544
FILING DATE: 03-OCT-1996
APPLICATION NUMBER: FR 95.11623
FILING DATE: 03-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 1487-20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-043-937A-2

Query Match 5.4%; Score 8; DB 3; Length 342;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 PAATAAA 71
DB 2 PAATAAA 9

RESULT 7
US-09-413-814-78
Sequence 78, Application US/09413814
Patent No. 6225064
GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Bloeker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polypeptide or
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 78
LENGTH: 882
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-413-814-78

Query Match 5.4%; Score 8; DB 3; Length 882;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 89 RAAAPPP 96

DB 336 RAAAPPP 343

RESULT 8
US-08-666-473-13
Sequence 13, Application US/08666473
Patent No. 5843713
GENERAL INFORMATION:
APPLICANT: YOSHIDA, Aruto
APPLICANT: TAKEUCHI, Makoto
TITLE OF INVENTION: PEPTIDE SEQUENCE THAT FORMS MUCIN SUGAR
TITLE OF INVENTION: CHAIN AND TECHNIQUE FOR MODIFYING PROTEIN TO BE LINKED
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/666,473
FILING DATE: 19-SEP-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP95/02238
FILING DATE: 01-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-22101
FILING DATE: 09-FEB-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 6-269111
FILING DATE: 01-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16887/837
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-666-473-13

Query Match 4.7%; Score 7; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 PAATAAA 70
DB 1 PAATAAA 7

RESULT 9
US-07-814-220-5
Sequence 5, Application US/07814220
Patent No. 5925540
GENERAL INFORMATION:
APPLICANT: Caceci, Thomas
APPLICANT: Toch, Thomas E.
APPLICANT: Szumanek, Maria B.W.

TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitlam, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-814-220-5

Query Match 4.7%; Score 7; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 65 AATAAA 71
|||
Db 2 AATAAA 8

RESULT 10
US-07-812-421-5
Sequence 5, Application US/07812421
Patent No. 5932697
GENERAL INFORMATION:
APPLICANT: Caceci, Thomas
APPLICANT: Toth, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitlam, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-812-421-5

Query Match 4.7%; Score 7; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 65 AATAAA 71
|||
Db 2 AATAAA 8

RESULT 11
US-09-117-121-2
Sequence 2, Application US/09117121
Patent No. 6307020
GENERAL INFORMATION:
APPLICANT: Hew, Choy
APPLICANT: Gong, Zhiyuan
TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
TITLE OF INVENTION: and Nucleic Acids
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/117,121
FILING DATE: 20-NOV-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CA97/00062
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 016252-001610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide
US-09-117-121-2

Query Match 4.7%; Score 7; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AATAAAA 71
1 AATAAAA 7

RESULT 12
US-07-814-220-27

Sequence 27, Application US/07814220
Patent No. 5925540

GENERAL INFORMATION:

APPLICANT: Cacaci, Thomas

APPLICANT: Toch, Thomas E.

APPLICANT: Szumanski, Maria B.W.

TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: WHITHAM, CURTIS & WHITHAM

STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,

STREET: Suite 900

CITY: Reston

STATE: VA

COUNTRY: USA

ZIP: 20191

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/814,220

FILING DATE: 23-DEC-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/588,437

FILING DATE: 25-SEP-1990

ATTORNEY/AGENT INFORMATION:

NAME: Whitham, Michael E.

REGISTRATION NUMBER: 32,635

REFERENCE/DOCKET NUMBER: CIT. 016

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-391-2510

TELEFAX: 703-391-9035

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-814-220-27

Query Match 4.7%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AATAAAA 71
1 AATAAAA 15

RESULT 13
US-07-812-421-27

Sequence 27, Application US/07812421
Patent No. 5932697
GENERAL INFORMATION:

APPLICANT: Cacaci, Thomas
APPLICANT: Toch, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900

CITY: Reston

STATE: VA

COUNTRY: USA

ZIP: 20191

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/812,421

FILING DATE: 23-DEC-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/588,437

FILING DATE: 25-SEP-1990

ATTORNEY/AGENT INFORMATION:

NAME: Whitham, Michael E.

REGISTRATION NUMBER: 32,635

REFERENCE/DOCKET NUMBER: CIT. 016

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-391-2510

TELEFAX: 703-391-9035

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-07-812-421-27

Query Match 4.7%; Score 7; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AATAAAA 71
9 AATAAAA 15

RESULT 14
US-07-814-220-24

Sequence 24, Application US/07814220
Patent No. 5925540

GENERAL INFORMATION:

APPLICANT: Cacaci, Thomas

APPLICANT: Toch, Thomas E.

APPLICANT: Szumanski, Maria B.W.

TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: WHITHAM, CURTIS & WHITHAM

STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900

CITY: Reston

STATE: VA

COUNTRY: USA

ZIP: 20191

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/814,220
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-814-220-24

Query Match 4.7%; Score 7; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AATPAAA 71
|||
8 AATPAAA 14

Db

RESULT 15
US-07-812-421-24
Sequence 24, Application US/07812421
Patent No. 5932697
GENERAL INFORMATION:
APPLICANT: Caceci, Thomas
APPLICANT: Toch, Thomas E.
APPLICANT: Szumanski, Maria B.W.
TITLE OF INVENTION: SYNTHETIC ANTIFREEZE PEPTIDE AND
TITLE OF INVENTION: SYNTHETIC GENE CODING FOR ITS PRODUCTION
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: WHITHAM, CURTIS & WHITHAM
STREET: Reston Intl. Center, 11800 Sunrise Valley Dr.,
STREET: Suite 900
CITY: Reston
STATE: VA
COUNTRY: USA
ZIP: 20191
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/812,421
FILING DATE: 23-DEC-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/588,437
FILING DATE: 25-SEP-1990
ATTORNEY/AGENT INFORMATION:
NAME: Whitham, Michael E.
REGISTRATION NUMBER: 32,635
REFERENCE/DOCKET NUMBER: CIT.016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-391-2510
TELEFAX: 703-391-9035
INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-812-421-24

Query Match 4.7%; Score 7; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 65 AATPAAA 71
|||
8 AATPAAA 14

Db

Search completed: January 30, 2004, 17:02:59
Job time : 26 secs

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OM protein - protein search, using sw model

Run on: January 30, 2004, 16:58:29 ; Search time 34 Seconds

(without alignments)
904.646 Million cell updates/sec

Title: US-09-809-545A-2_COPY_1_148
Perfect score: 148
Sequence: 1 MTNKKAVNPYTNQWKLNPV.....PATAAAYSDSYGRVYAADPY 148

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Gapco 60.0 , Gapext 60.0

Searched: 789580 seqs, 207824079 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

Database :

Published Applications_AA:*

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- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
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- 9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
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- 15: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	148	100.0	203	10	US-09-809-545A-2
2	57	38.5	330	9	US-09-794-591-2
3	13	8.8	366	12	US-10-359-385-2
4	13	8.8	450	10	US-10-094-749-1926
5	8	5.4	325	12	US-09-736-457-1816
6	8	5.4	325	10	US-09-902-941-1816
7	8	5.4	325	10	US-09-849-626-1816
8	8	5.4	325	12	US-10-113-872-1816
9	8	5.4	325	12	US-10-382-600-28
10	8	5.4	325	15	US-10-017-754-1816
11	8	5.4	342	9	US-09-833-790-236
12	8	5.4	342	15	US-10-177-293-246
13	8	5.4	340	15	US-10-207-653-198
14	8	5.4	633	14	US-10-086-464-11
15	8	5.4	674	15	US-10-156-761-9618

16	8	5.4	708	12	US-10-382-600-29	Sequence 29, Appl
17	7	4.7	19	9	US-09-864-761-35418	Sequence 35418, A
18	7	4.7	72	9	US-09-864-761-33368	Sequence 33368, A
19	7	4.7	92	10	US-09-966-546-24	Sequence 24, Appl
20	7	4.7	92	10	US-09-966-545-24	Sequence 24, Appl
21	7	4.7	92	11	US-09-965-212-24	Sequence 24, Appl
22	7	4.7	92	16	US-10-189-940-24	Sequence 104, Appl
23	7	4.7	105	12	US-10-191-813-104	Sequence 24, Appl
24	7	4.7	105	12	US-10-191-813-106	Sequence 106, App
25	7	4.7	105	12	US-10-191-813-108	Sequence 106, App
26	7	4.7	105	12	US-10-191-813-110	Sequence 110, App
27	7	4.7	105	12	US-10-191-813-112	Sequence 112, App
28	7	4.7	105	12	US-10-191-813-114	Sequence 114, App
29	7	4.7	105	12	US-10-191-813-116	Sequence 116, App
30	7	4.7	105	12	US-10-191-813-118	Sequence 118, App
31	7	4.7	116	9	US-09-867-550-1068	Sequence 1068, Ap
32	7	4.7	117	12	US-10-029-386-13868	Sequence 3368, A
33	7	4.7	132	9	US-09-864-761-37187	Sequence 37187, A
34	7	4.7	133	14	US-10-062-254-150	Sequence 150, App
35	7	4.7	147	9	US-09-864-761-38175	Sequence 38175, A
36	7	4.7	157	10	US-09-764-864-1325	Sequence 1325, Ap
37	7	4.7	189	9	US-09-810-264-20	Sequence 20, Appl
38	7	4.7	203	12	US-10-258-666-6	Sequence 6, Appl
39	7	4.7	203	15	US-10-156-761-13350	Sequence 13350, A
40	7	4.7	221	10	US-09-738-626-5334	Sequence 5334, Ap
41	7	4.7	261	15	US-10-043-487-220	Sequence 220, App
42	7	4.7	263	15	US-10-156-761-9572	Sequence 9572, Ap
43	7	4.7	272	12	US-10-174-209-24	Sequence 24, Appl
44	7	4.7	282	15	US-10-102-806-478	Sequence 478, App
45	7	4.7	287	15	US-10-176-847-66	Sequence 66, Appl

ALIGNMENTS

RESULT 1
US-09-809-545A-2
; Sequence 2, Application US/09809545A
; Patent No. US20020110804A1
; GENERAL INFORMATION:
; APPLICANT: Stanton, Lawrence W.
; APPLICANT: White, R. Tyler
; TITLE OF INVENTION: SECRETED FACTORS
; FILE REFERENCE: SCIOS 017A
; CURRENT APPLICATION NUMBER: US/09/809,545A
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-09-809-545A-2

Query Match 100.0%; Score 148; DB 10; Length 203;

Best Local Similarity 100.0%; Pred. No. 3.6e-127;

Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTNKKAVNPYTNQWKLNPVGVAVSPDFAAGTYLLCQANQEGSSMYSGPSSLVYTSAMPG 60	
DB	1	MTNKKAVNPYTNQWKLNPVGVAVSPDFAAGTYLLCQANQEGSSMYSGPSSLVYTSAMPG 60	
QY	61	FPYPAATAAARGAHLRGRGRTVNTFPFAAAPPIPAVGIVYQEPYGNKLLGGYA 120	
DB	61	FPYPAATAAARGAHLRGRGRTVNTFPFAAAPPIPAVGIVYQEPYGNKLLGGYA 120	
QY	121	AVRYAQTPTATAAAYSDSYGRVYAADPY 148	
DB	121	AVRYAQTPTATAAAYSDSYGRVYAADPY 148	

RESULT 2
US-09-794-591-2

Sequence 2, Application US/09794591
Patent No. US20010018198A1
GENERAL INFORMATION:
APPLICANT: Pulset, Stefan M.
APPLICANT: Shibata, Hiroki
TITLE OF INVENTION: Nucleic Acids Encoding Ataxin-2 Binding Proteins,
Products Related Thereto and Methods of Using Same
FILE REFERENCE: CE 3093
CURRENT APPLICATION NUMBER: US/09/794,591
CURRENT FILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 09/145,391
PRIOR FILING DATE: 1998-09-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-09-794-591-2

Query Match 38.5%; Score 57; DB 9; Length 330;
Best Local Similarity 100.0%; Pred. No. 5.8e-44;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 PSSLVYTSAMGFPYPAATAAAVRGAHLRGRGRTVNTFPAAPPPPIPGGVY 105
DB 244 PSSLVYTSAMGFPYPAATAAAVRGAHLRGRGRTVNTFPAAPPPPIPGGVY 300

RESULT 3
US-10-359-385-2
Sequence 2, Application US/10359385
Patent No. US20030143622A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Guesgler, Karl J.
APPLICANT: Lu, Aina
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN RNA BINDING PROTEINS
FILE REFERENCE: PP-0611 US
CURRENT APPLICATION NUMBER: US/10/359,385
CURRENT FILING DATE: 2003-02-05
PRIOR APPLICATION NUMBER: US/09/176,657
PRIOR FILING DATE: 1998-10-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PERL Program
SEQ ID NO 2
LENGTH: 366
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: 1250374
US-10-359-385-2

Query Match 8.8%; Score 13; DB 12; Length 366;
Best Local Similarity 100.0%; Pred. No. 0.00089;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 RGAHLRGRGRTVY 85
DB 267 RGAHLRGRGRTVY 279

RESULT 4
US-10-094-749-1926
Sequence 1926, Application US/10094749
Patent No. US20030219741A1
GENERAL INFORMATION:
APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI

APPLICANT: MAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOMYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1926
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-1926

Query Match 8.8%; Score 13; DB 12; Length 450;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 RGAHLRGRGRTVY 85
DB 341 RGAHLRGRGRTVY 353

RESULT 5
US-09-736-457-1816
Sequence 1816, Application US/09736457
Patent No. US20020168637A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darlick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1816
LENGTH: 325
TYPE: PRT
ORGANISM: Homo sapiens
US-09-736-457-1816

Query Match 5.4%; Score 8; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 AAAPPPPI 97

Db 67 AAAPPPPI 74

RESULT 6

US-09-902-941-1816
; Sequence 1816, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1816
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-1816

Query Match 5.4%; Score 8; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 AAAPPPPI 97
Db 67 AAAPPPPI 74

RESULT 7

US-09-849-626-1816
; Sequence 1816, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tongtong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1816
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-626-1816

Query Match 5.4%; Score 8; DB 10; Length 325;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 90 AAAPPPPI 97
Db 67 AAAPPPPI 74

Db 67 AAAPPPPI 74

RESULT 8

US-10-113-872-1816
; Sequence 1816, Application US/10113872
; Publication No. US20030170255A1
; GENERAL INFORMATION:
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C19
; CURRENT APPLICATION NUMBER: US/10/113,872
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 2011
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1816
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-113-872-1816

Query Match 5.4%; Score 8; DB 12; Length 325;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 AAAPPPPI 97
Db 67 AAAPPPPI 74

RESULT 9

US-10-382-600-28
; Sequence 28, Application US/10382600
; Publication No. US20030219799A1
; GENERAL INFORMATION:
; APPLICANT: Horriagan, Stephen
; APPLICANT: Young, Paul
; APPLICANT: Eber, Reinhard
; TITLE OF INVENTION: Cancer-Linked Gene as Target for Chemotherapy
; FILE REFERENCE: 689290-127
; CURRENT APPLICATION NUMBER: US/10/382,600
; CURRENT FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: US 60/362,419
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-382-600-28

Query Match 5.4%; Score 8; DB 12; Length 325;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 AAAPPPPI 97
Db 67 AAAPPPPI 74

RESULT 10
US-10-017-754-1816
; Sequence 1816, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:

APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tonglong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Marnerakis, Margarita
APPLICANT: Carter, Darick
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McInabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C18
CURRENT APPLICATION NUMBER: US/10/017,754
CURRENT FILING DATE: 2001-10-29
NUMBER OF SEQ ID NOS: 2004
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1816
LENGTH: 325
TYPE: PRT
ORGANISM: Homo sapiens
US-10-017-754-1816

Query Match 5.4%; Score 8; DB 15; Length 325;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 90 AAAPPPPI 97
Db 67 AAAPPPPI 74

RESULT 11
US-09-833-790-236
Sequence 236, Application US/09833790
Patent No. US20020068288A1
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Wang, Tonglong
APPLICANT: Secrist, Heather
APPLICANT: Monamach, Radoch
APPLICANT: Indirias, Carol Y.
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 236
LENGTH: 342
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-790-236

Query Match 5.4%; Score 8; DB 9; Length 342;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 90 AAAPPPPI 97
Db 84 AAAPPPPI 91

RESULT 12
US-10-177-293-246
Sequence 246, Application US/10177293
Publication No. US20030124128A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Glatt, Karen

APPLICANT: Zhao, Xumei
APPLICANT: Gannavarpu, Manjula
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Mertens, Maureen
APPLICANT: Myer, Vic
APPLICANT: Wang, Youzhen
APPLICANT: Xu, Yongyao
APPLICANT: Hoersch, Sebastian
APPLICANT: Monahan, John
APPLICANT: Meyers, Rachel E.
APPLICANT: Bast Jr., Robert C.
APPLICANT: Hortobagyi, Gabriel N.
APPLICANT: Pusztai, Lajos
APPLICANT: Meric, Funda
APPLICANT: Sahin, Aysegül
APPLICANT: Mills, Gordon B.
TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
FILE REFERENCE: MFI-038
CURRENT APPLICATION NUMBER: US/10/177,293
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: US 60/299,887
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: US 60/301,572
PRIOR FILING DATE: 2001-06-27
PRIOR APPLICATION NUMBER: US 60/306,501
PRIOR FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: US 60/325,002
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US 60/362,585
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/xxx,xxx
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 506
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 246
LENGTH: 342
TYPE: PRT
ORGANISM: Homo sapiens
US-10-177-293-246

Query Match 5.4%; Score 8; DB 15; Length 342;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 90 AAAPPPPI 97
Db 84 AAAPPPPI 91

RESULT 13
US-10-207-655-198
Sequence 198, Application US/10207655
Publication No. US20030118592A1
GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390659.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: PatentIn version 3.0
SEQ ID NO 198
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-10-207-655-198

Query Match 5.4%; Score 8; DB 15; Length 540;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 64 PAATMAA 71
 Db 484 PAATMAA 491

Db 308 RAAAPPP 315
 Search completed: January 30, 2004, 17:01:53
 Job time : 42 secs

RESULT 14
 US-10-086-464-11
 ; Sequence 11, Application US/10086464
 ; Publication No. US20020199218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GORING, Daphne R. et al.
 ; TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
 ; FILE REFERENCE: P 25, 762-A USA
 ; CURRENT APPLICATION NUMBER: US/10/086,464
 ; CURRENT FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 10/069,304
 ; PRIOR FILING DATE: 2002-02-19
 ; PRIOR APPLICATION NUMBER: PCT/CA00/00966
 ; PRIOR FILING DATE: 2000-08-18
 ; PRIOR APPLICATION NUMBER: US 60/149,466
 ; PRIOR FILING DATE: 1999-08-19
 ; PRIOR APPLICATION NUMBER: US 60/159,122
 ; PRIOR FILING DATE: 1999-10-13
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 11
 ; LENGTH: 633
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-086-464-11

Query Match 5.4%; Score 8; DB 14; Length 633;
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 SSMYSGPS 50
 Db 245 SSMYSGPS 252

RESULT 15
 US-10-156-761-9618
 ; Sequence 9618, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMIURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI
 ; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 9618
 ; LENGTH: 674
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis
 US-10-156-761-9618

Query Match 5.4%; Score 8; DB 15; Length 674;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 89 RAAAPPP 96
 |||||

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